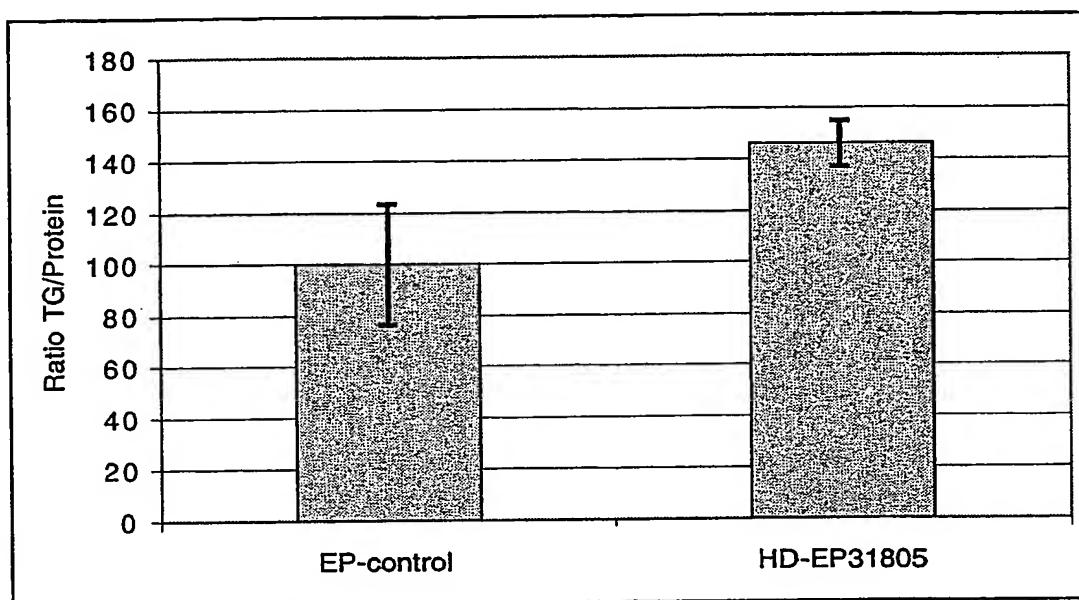


Figure 1. Triglyceride content of a Drosophila CG7956 (GadFly Accession Number) mutant



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Figure 2. Molecular organization of the CG7956 gene (GadFly Accession Number)

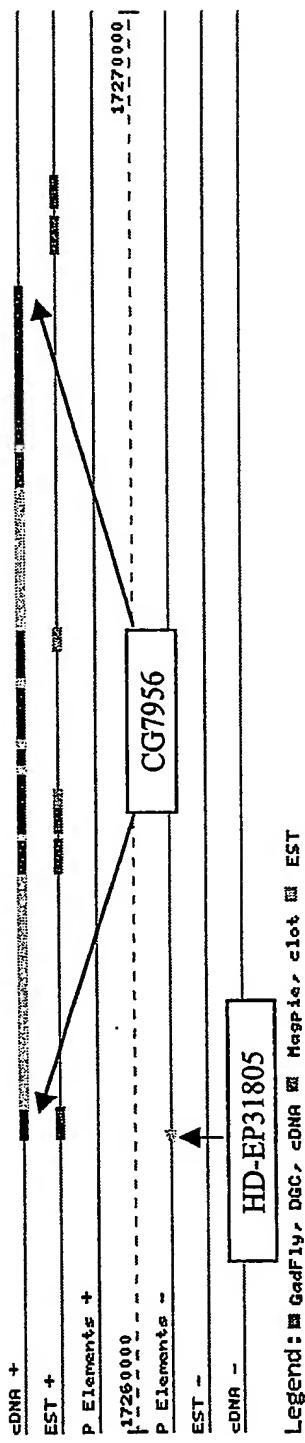


Figure 3. BLASTP results for CG7956 (GadFly Accession Number)**Homology to human protein NP_055752.1 (GenBank Accession Number)**

ref|NP_055752.1| (NM_014937) KIAA0966 protein [Homo sapiens]
Length = 1132

Score = 573 bits (1477), Expect = e-162
Identities = 354/972 (36%), Positives = 514/972 (52%), Gaps = 114/972 (11%)

Query: 1 MEVFQTDSHYIFVKRDKSLWWHRRTSEFSIKAGWDLSSVDDIECIGVTHGIVGVISLPNV 60
ME+FQ HYI + +++LW RR ++ DL + C+G+ G++G I L +
Sbjct: 1 MELFQAKDHYILOQGERALWCSSRGGQLQRPATDLLLAWNPICLGLVEGVIGKIQHLHSD 60

Query: 61 YEPHLVVVKEASAVGVLYPPHLVYKIKSICILSADD---PDTDLPNCTKHTKSNQSTPTH 117
L+++++ + VG L H V K+ I +LS + D +L C KH
Sbjct: 61 LPWWLILIRQKALVGKLPGDHEVCKVTKIAVLSLSEMEEPQDLELELCKKH----- 110

Query: 118 SVSTSNNNNASVPSSGGSSKSTKLFEGMNKWTGAVKSAGNT---IKNTTQQAANLATKQ 174
G+NK + S ++ +K T +N++
Sbjct: 111 -----HFGINKPEKIIIPSPDDSKFLKTFTHIKSNVSAPN 145

Query: 175 VKSSVGIREPRHIERRITEELHKIFDETDSFYFSFDCTITNNLQRHEAKSEESQ---SQP 231
K +E +ERR+ EEL K+F +++SFY+S D+TN++QR + + +
Sbjct: 146 KKKVKESKEKEKLERRLLEELLKMFMDSESFYYSLTYDLTNSVQRQSTGERDGRPLWQKV 205

Query: 232 DERFFWNKHMIRDLINLNDKT---WILPIIQGFMQVENCVIG----- 270
D+RFFWNK+MI+DL + WI+P+IQGF+Q+E V+
Sbjct: 206 DDRFFWNKYMIQDLTEIGTPDVDFWIIPMIQGFVQIEELVVNYTESSDDEKSSPETPPQE 265

Query: 271 NEC-----FTLALVSRSSRHAGTRYKRRGVDEKGNCANYVETEQILSFRHHQLSFTQ 323
+ C F +AL+SRRSRHAG RYKRRGV+ GN ANYVETEQ++ +H LSF Q
Sbjct: 266 STCVDDIHPRFLVALISRRSRHAGMRYKRRGVDKNGNVANYVETEQLIHVHNHTLSFVQ 325

Query: 324 VRGSVPPIYWSQPGKYRPPPRLDRGVAETQQAFELHFTKELETYGRVCIVNLVEQSGKEK 383
RGGSVP++WSQ GY+Y P PRLDR ET F HF ++L Y + I+NLV+Q+G+EK
Sbjct: 326 TRGSVPVFWSQVGYRYNPRPRLDRSEKETVAYFCAHFEEQLNIYKKQVIINLVDQAGREK 385

Query: 384 TIGDAYADHVIKLNNDRLIYVTDFHDYCRGMRFENVSALIDAVGPEAGAMGFHWRDQRG 443
IGDAY V+ NN L YV+FDFH++CRGM+FENV L DA+ M + W D+ G
Sbjct: 386 IIIGDAYLKQVLLFNNSHLYVSFDHEHCRCMKFENVQTLDAIYDIILDMKWCWVDEAG 445

Query: 444 MICNQKSFRVNCMDCLDRTNVQTAIGKAVLESQVLKGLSPPYTPPIPEQLKSPFMVLW 503
+IC Q+ +FRVNCMDCLDRTNVQ AI + V+E QL KLG+ PP P+P + + ++W
Sbjct: 446 VICKQEGIFRVNCMDCLDRTNVQAAIARVVMEQQLKKGMPPEQPLPVKCNRIYQIMW 505

Query: 504 ANNGDIISROYAGTNALKGDYTRTGERKISGMMKDGMNSANRYYLARFKDSYRQATIDL 563
ANNGD ISROQYAGT ALKGD+TRTGERK++G+MKDG+NSANRYYL RFKD+YRQA IDLM
Sbjct: 506 ANNGDSISRQYAGTAALKGDFTRTGERKLAGVMKDGVNSANRYYLNRFKDAYRQAVIDLM 565

Query: 564 LGNQVSSESLSALGGQAGPD---ENDGTENAEQAKLLVEDCRRLLLGTQYVGAWLID 620
G V+ + S + + + + E L++ +LLL + G W LID
Sbjct: 566 QGIPVTEDLYSIFTKEKEHEALHKENQRSHQELISQLLQSYMKLLL PDDEKFHGGWALID 625

Query: 621 ADPSSGDINETEVDTILLTDDCYIVAHEYDSHLDKIVRFEKVQLTVRLIELGMHQQT 680
DPS D +VD +LLL++ Y VA YD +DK+ +++++ L + IE+G + +
Sbjct: 626 CDPSSLIDATHRDVDVLLLSNSAYYVAYYDDEVDKVNQYQRLSLENLEKIEIG--PEPTL 683

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WO 03/092715

PCT/EP03/04650

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Query: 681 FQGSAPAHLCRLNYSVDEQEGLYFHMFRSANLRFFNNMAYVIKTQEEVAESMTSIVEMFR 740
F P C+RL+Y E GYFH R A + +E+ +++ I EM +
Sbjct: 684 F--GKPKFSCMRLHYRYKEASGYFHTLR-----AVMRNPEEDGKDTLQCIAEMLQ 731

Query: 741 IALDNAGNTEVRYITGGVLQRRKSKLPTLDV-----PRGMPRNLSSEQLVQLSSKA 791
I G+ I L+R+ SK P D+ +N S+ L+ K
Sbjct: 732 ITKQAMGSD--LPIIEKKLERKSSK-PHEDIIGIRSQNQGSLAQGKNFLMSKFSSLNQKV 788

Query: 792 LSNMA----GQFSKLGQTFKKPQAHPSSLAATMNPQVMRQRDSEIESGQEAEKAVFTLGR 847
+ G KLG F KP+ + L + + + DS +E+ + V +
Sbjct: 789 KOTKSNVNIGNLRKLG-NFTKPEMKVNFLKPNLKVNWLKS-DSSLETMENT--GVMDKVQ 844

Query: 848 KHRNSNSASSTDTEHDNSLYEPEVDSDVEIAMDKSNYNE-NAFLPSVGIVMG---NQK 902
+ + +S D+ D L + D D ++A + + LPS GI+ +
Sbjct: 845 AESDGDMSSDNDSYHSDEFLTNSKSDEDRQLANSLESVGPIDYVLPSCGIIASAPRLGSR 904

Query: 903 EDSPSSSDEIRH 914
S SS+D H

Sbjct: 905 SQSLSSTDSSVH 916

Figure 4. Expression of the CG7956 Homologs in Mammalian Tissues

Figure 4A. Real-time PCR analysis of Sac domain-containing inositol phosphatase 2 (SAC2) expression in wild type mouse tissues

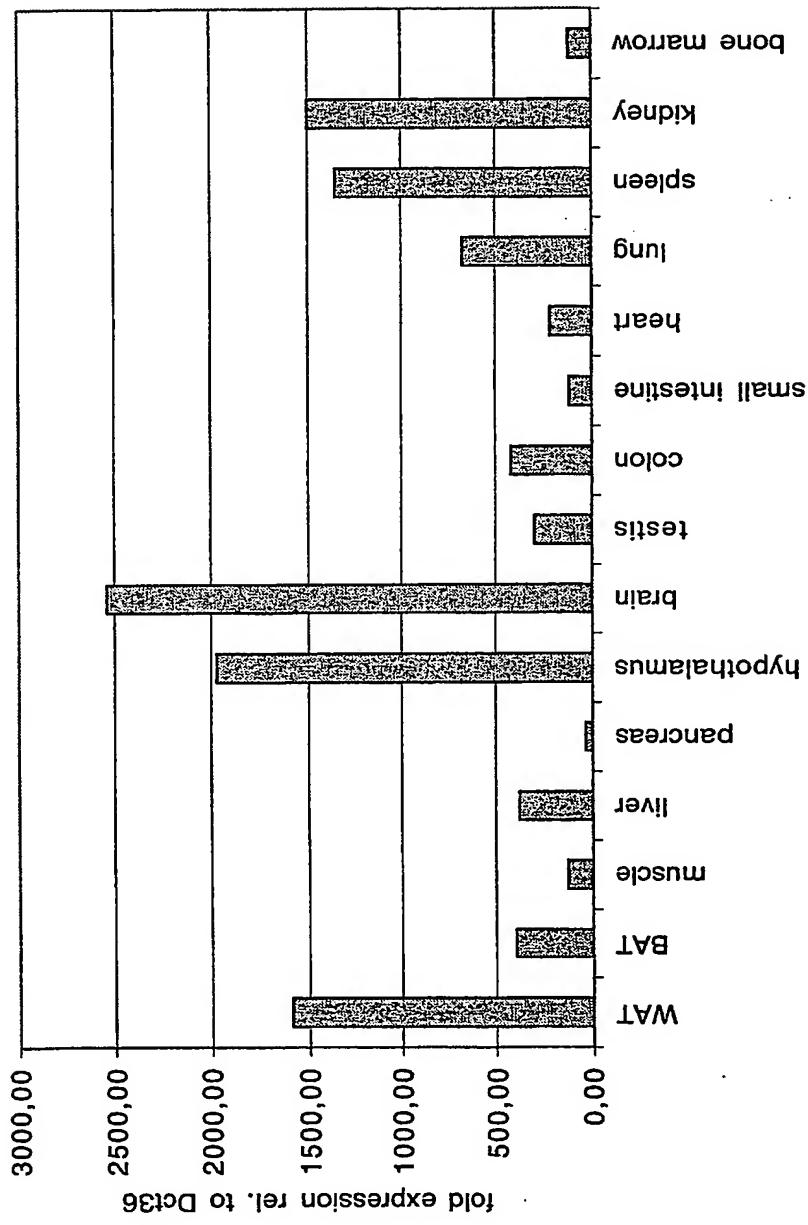


Figure 4B. Real-time PCR analysis of Sac domain-containing inositol phosphatase 2 (SAC2) expression in different mouse models

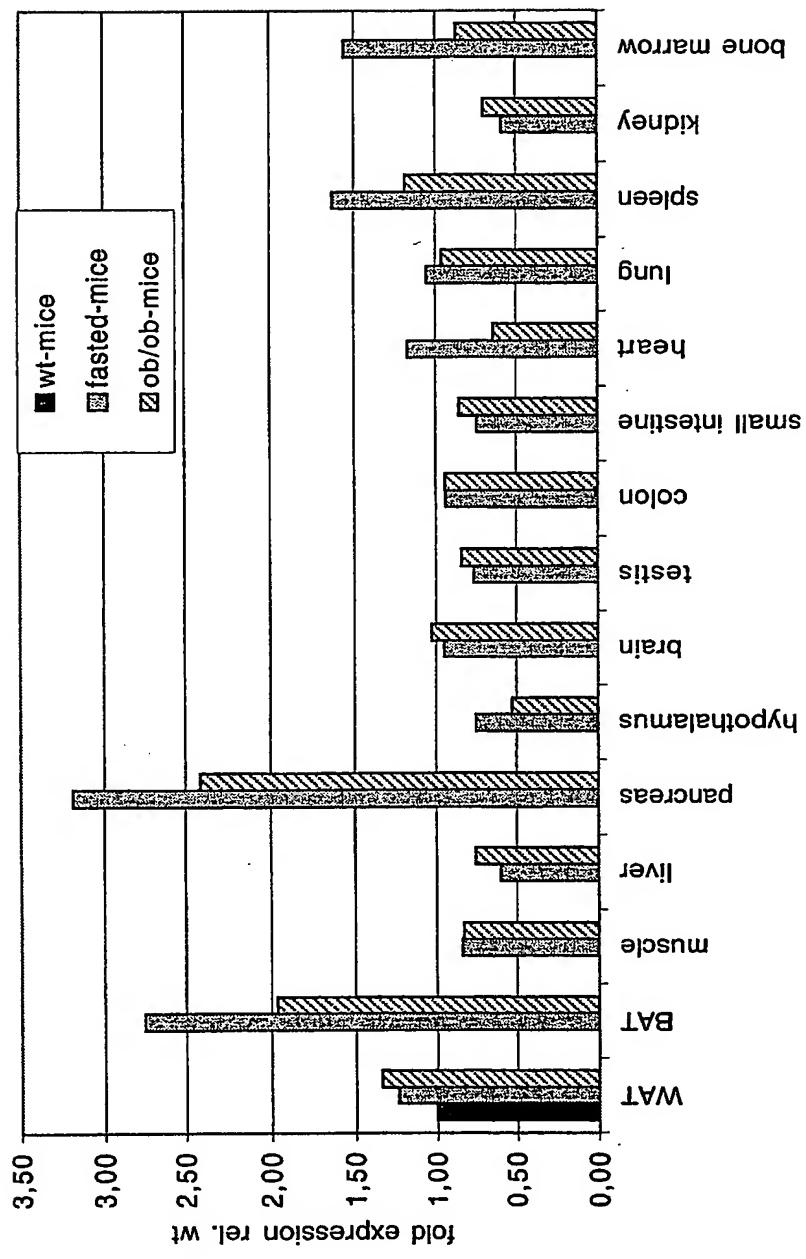


Figure 5. Triglyceride content of a *Drosophila aralar 1* (GadFly Accession Number CG2139) mutant

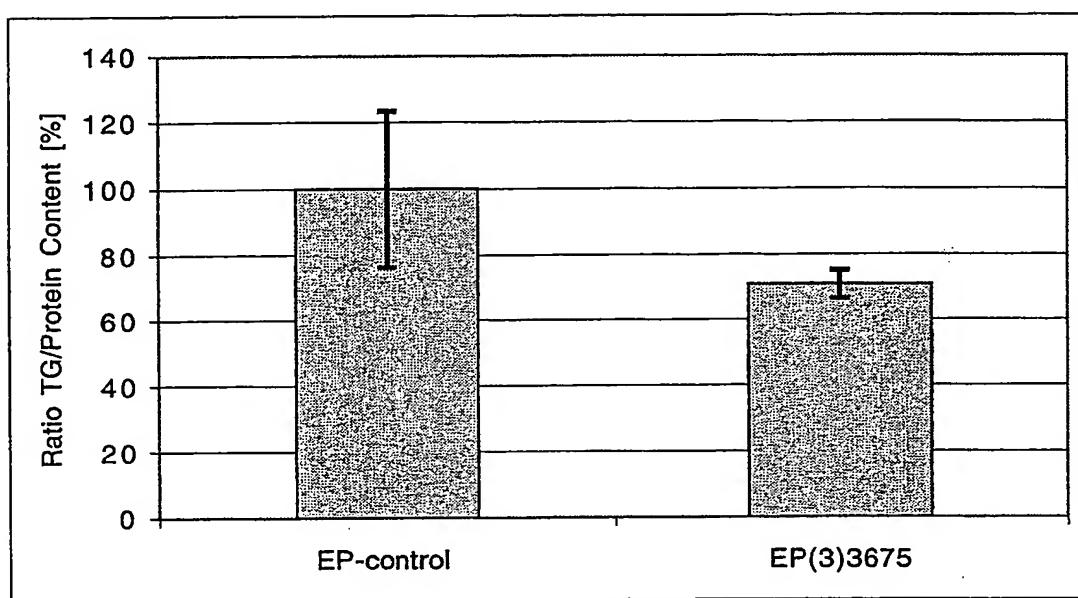


Figure 6. Molecular organisation of the *aralard* 1 gene (GadFly Accession Number CG2139)

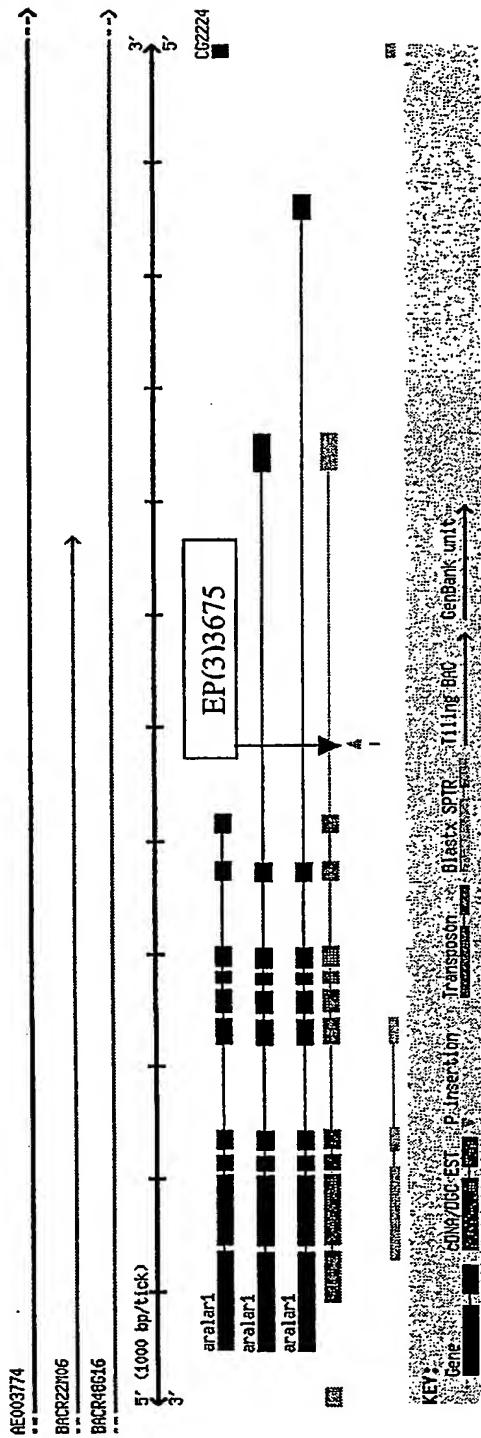


Figure 7. Homology of *Drosopila aralar 1* (GadFly Accession Number CG2139) to human solute carrier family 25, members 12 and 13

**Figure 7A. BLASTP results for *aralar 1*
Homology to human protein XP_010876.3 (GenBank Accession Number)**

ref|XP_010876.3| (XM_010876) solute carrier family 25 (mitochondrial carrier, Aralar), member 12 [Homo sapiens]
Length = 678

Score = 741 bits (1913), Expect = 0.0
Identities = 382/650 (58%), Positives = 488/650 (74%), Gaps = 14/650 (2%)

Query: 1 MTSEDFVRKPLGLFSESAFNDESVRLLANIADTSKDGLISFSEFOAFEGLLCTPDALYRT 60
MT EDFV+++LGL+++ N + V+LLA +AD +KDGTLIS+ EF AFE +LC PD+++
Sbjct: 34 MTPEDFVQRYLGLYNDPNSNPKIVQLLAGVADQTKDGLISYQEFLAFESVLCAPDSMFIV 93

Query: 61 AFQLFDRKGNGTVSYADFADVVQKTELHSKIPFSLDGPFIKRYFGDKKKQRLINYAFTQL 120
AFQLFD+ GNG V++ + ++ +T +H IPF+ D FI+ +FG +++ +NY EFTQ
Sbjct: 94 AFQLFDKSGNGEVTFENVKEIFGQTIIHHHIPNWDCEFIRLHFHNRKKHLNYTEFTQF 153

Query: 121 LHDFHEEHAMEAFRSKDPAGTGFISPLDFQDIIVNVKRHLLTPGVRDNLVSVTEG---HK 177
L + EHA +AF KD + +G IS LDF DI+V ++ H+LTP V +NLVS G H+
Sbjct: 154 LQELQLEHARQAFALKDKSKSGMISGLDFS DIMVTIRSHMLTPFVEENLVSAAGGSISHQ 213

Query: 178 VSFPYFIAFTSLLNNMELIKQVYLHATEGSRTDM-ITKDQILLAAQTMSQITPLEIDILF 236
VSF YF AF SLLNNMEL++++Y G+R D+ +TK++ +A Q+TPLEIDIL+
Sbjct: 214 VSFSYFNANFSLLNNMELVRKIY-STLAGTRKDVEVTKEEFAQSAIRYQGQVTPLEIDILY 272

Query: 237 HLAGAVHQAGRIDLSDLSNIAPEHYTKHMTHRLAEIKAVESPA-DRSAFIQVLESSYRFT 295
LA + +GR+ +D+ IAP + + LAE++ +SP R ++Q+ ES+YRFT
Sbjct: 273 QLADLYNASGRRTLADIERIAPLAEGA-LPYNLAEQRRQQSPGLGRPIWLQIAESAYRFT 331

Query: 296 LGSFAGAVGATVVYPIDLVKTRMQNQR-AGSYIGEVAYRNSWDCFKVVRHEGMGLYRG 354
LGS AGAVGAT VYPIDLVKTRMQNQR +GS +GE+ Y+NS+DCFKKV+R+EGF GLYRG
Sbjct: 332 LGSVAGAVGATAVVYPIDLVKTRMQNQRGSGSJVGELMYKNSFDCFKVLRYEGFFGLYRG 391

Query: 355 LLPQLMGVAPEKAIKLTVDLVRDKLTDKGNIPPTWAEVLAGGCAGASQVVFTNPLEIVK 414
L+PQL+GVAPEKAIKLTVD VRDK T + G++P AEVLAGGCAG SQV+FTNPLEIVK
Sbjct: 392 LIPOQLIGVAPEKAIKLTVDLVRDKFTRRDGSVPLPAEVLAGGCAGGSQVIFTNPLEIVK 451

Query: 415 IRLQVAGEIASGSKIRAWSVVERLGLGLYKGARACLLRDVPFSAIYFPTYAHTKAMMAD 474
IRLQVAGEI +G ++ A +V+R+LG+FGLYKGA+AC LRD+PFSAIYFP YAH K ++AD
Sbjct: 452 IRLQVAGEITTGPRVSALNVLRLDLGIFGLYKGAKACFLRDIPFSAIYFPVYAHCKLLLAD 511

Query: 475 KDGYNHPLTLLAAGAIAGVPAASLVT PADVIKTRLQVVARSGQTTYTGVWDATKKIMAAE 534
++G+ L LLAAGA+AGVPAASLVT PADVIKTRLQV AR+GQTTY+GV D +KI+ EE
Sbjct: 512 ENGHVGGLNLLAAGAMAGVPAASLVT PADVIKTRLQVAARAGQTTYSGVIDCFRKILREE 571

Query: 535 GPRAFWKGTAARVFRSSPQFGVTLVTYELLQRLFYVDFGGTQPKGSEAHKITTPLEQAAA 594
GP AFWKGTAARVFRSSPQFGVTLVTYELLQR FY+DFGG +P GSE TP + A
Sbjct: 572 GPSAFWKGTAAARVFRSSPQFGVTLVTYELLQRWFYIDFGGLKPAGSE---PTP-KSRIA 626

Query: 595 SVTENVDHIGGYRAAVPLLALGVESKFLYLPFR-GRGVTAASPSTATGS 643
+ N DHIGGYR A AG+E+KFLYLP+F V P A +
Sbjct: 627 DLPPANPDHIGGYRLATATFAGIENKFGLYLPKFKSPSVAVVQPKAAVAA 676

Homology to human protein NP_055066.1 (GenBank Accession Number)

ref|NP_055066.1| (NM_014251) solute carrier family 25, member 13 (citrin)
[Homo sapiens]
Length = 675

Score = 728 bits (1878), Expect = 0.0
Identities = 374/643 (58%), Positives = 476/643 (73%), Gaps = 17/643 (2%)

Query: 1 MTSEDFVRKFLGLFSESAFNDESVRLLANIADTSKDGLISFSEFQAFEGLLCTPDALYRT 60
M+ DFV ++L +F ES N ++V LL+ + D +KDGLISF EF AFE +LC PDAL+
Sbjct: 35 MSPNDFVTRYLNIFGESQPNPKTVELLSGVVDQTKDGLISFQEFAFESVLCAPDALFMV 94

Query: 61 AFQLFDRKGNGTVSYADFADVVKETELHSKIPFSLDGPFIKRYFGDKKQRLINYAEFTQL 120
AFQLFD+ G G V++ D V +T +H IPF+ D F++ +FG +++R + YAEFTQ
Sbjct: 95 AFQLFDKAGKGEVTFEDVKQVFGQTTIHQHIPFNWDSEFVQLHFGKERKRHLTYAEFTQF 154

Query: 121 LHDFHEEHAMEAFRSKDPAGTGFISPLDFQDIIVNVKRHLLPGVRDNLVSYTEG---HK 177
L+ EHA +AF +D A TG ++ +DF+DI+V ++ H+LTP V + LV+ G H+
Sbjct: 155 LLEIQLEHAKQAFVQRDNARTGRVTAIDFRDIMVTIRPHVLTPFVEECLVAAAGGTTSHQ 214

Query: 178 VSFPYFIAFTSLLNNMELIKQVYLHATEGSRTDM-ITKDQILLAAQTMSQITPLEIDILF 236
VSF YF F SLLNNMELI+++Y G+R D+ +TK++ +LAAQ Q+TP+E+DILF
Sbjct: 215 VSFSYFNGFNSLLNNMELIRKIY-STLAGTRKDVEVTKEEFVLAAQKFGQVTPMEVDILF 273

Query: 237 HLAGAVHQAGRIDLSDLSNIAP-EHYTKHMTHRLAEIKAVESPAD--RSAFIQVLESSYR 293
LA GR+ +D+ IAP E T + LAE + ++ D R +QV ES+YR
Sbjct: 274 QLADLYEPRGRMTLADIERIAPLEEGT--LPFNLAEAQRQKASGDSARPVLLQVAESAYR 331

Query: 294 FTLGSFAGAVGATVVYPIDLVKTRMQNORA-GSYIGEVAYRNSWDCFKVVRHEGMGLY 352
F LGS AGAVGAT VYPIDLVKTRMQNOR+ GS++GE+ Y+NS+DCFKKV+R+EGF GLY
Sbjct: 332 FGLGSVAGAVGATAVYPIDLVKTRMQNQRSTGSFVGELMYKNSFDCFKVLRYEGFFGLY 391

Query: 353 RGLLPQLMGVAPEKAIKLTVNDLVRDKLTDKGNIPWTAEVLAGGCAGASQVVFTNPLEI 412
RGLLPQL+GVAPEKAIKLTVND VRDK K G++P AE+LAGGCAG SQV+FTNPLEI
Sbjct: 392 RGLLPQLLGVAPEKAIKLTVNDFVRDKFMHKDGSVPLAETLAGGCAGGSQVIFTNPLEI 451

Query: 413 VKIRLQVAGEIASGSKIRAWSVVRELGLFGLYKGARACLLRDVPFSAIYFPTYAHTKAMM 472
VKIRLQVAGEI +G ++ A SVVR+LG FG+YKGA+AC LRD+PFSAIYFP YAH KA
Sbjct: 452 VKIRLQVAGEITTGPRVSALS VVRDLGFFGIYKGAKACFLRDIPFSAIYFPCYAHVKASF 511

Query: 473 ADKDGYNHPLTLLAAGAIAGVPAASLVTPADVIKTRLQVVARSGQTTYTGVDATKKIMA 532
A++DG P +LL AGAIAG+PAASLVTPADVIKTRLQV AR+GQTTY+GV D +KI+
Sbjct: 512 ANEDGQVSPGSLLL AGAIAGMPAASLVTPADVIKTRLQVAARAGQTTYSGVIDCFRKILR 571

Query: 533 EEGPRAFWKGTAARVFRSSPQFGVTLVTYELLQRLFYVDFGGTQPKGSEAHKITTPLEQA 592
EEGP+A WKG ARVFRSSPQFGVTL+TYELLQR FY+DFGG +P GSE P+ ++
Sbjct: 572 EEGPKALWKAGARVFRSSPQFGVTLTYELLQRWFYIDFGGVKPMGSE-----PVPKS 625

Query: 593 AASVTTENVDHIGGYRAAVPLLLAGVESKFGGLYLPRFGRGVTA 635
++ N DH+GGY+ AV AG+E+KFGGLYLP F V+ +
Sbjct: 626 RINLPAPNPDHVGGYKLAVATFAGIENKFGLYLPFLFKPSVSTS 668

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WO 03/092715

PCT/EP03/04650

11/51

Figure 7B. Multiple Sequence Alignment (ClustalW 1.83)

aralar1 Dm MPLTKSLPNPSLLKРАГТЕKLREVFLKYASIQKNGEHYMTSEDFVRKFLGLFSESAFND
SLC25A12 Hs -----MAVKVQTTKRGDPHELRNIFLQYASTEVGDGERYMPEDFVQRYLGLYNDPNSNP
SLC25A13 Hs -----MAAAKVALTKRADPAELRTIFLKYASIEKNGEFFMSPNDFVTRYLNIFGESQPNP

aralar1 Dm ESVRLLANIADTSKDGLISFSEFQAFEGLLCTPDALYRTAFQLFDRKGNGTVSYADFADV
SLC25A12 Hs KIVQLLAGVADQTKDGLISYQEFLAFESVLACPDMSFIVAFQLFDKSGNGEVTFENVKEI
SLC25A13 Hs KTVELLSGVVVDQTKDGLISFQEFAFESVLACPDALFMVAFQLFDKAGKGEVTFEDVKV

aralar1 Dm VQKTELHSKIPFSLDGPFIKRYFGDKKQRLINYAEFTQLLHDFHEEHAMEAFRSKDPAGT
SLC25A12 Hs FGQTIIHHHIPFNWDCEFIRLHFHNRKKHLNYTEFTQFLQELQLEHARQAFALKDKSKS
SLC25A13 Hs FGQTIIHQHIPFNWDSEFVQLHFGKERKRHLTYAEFTQFLLEIQLEHAQAFVQRDNART

aralar1 Dm GFISPLDFQDIIIVNVKRHLLTPGVRDNLVSVTAG---HKVSFPYFIAFTSLLNNMELIKQ
SLC25A12 Hs GMI SGLDFSDIMVTIRSHMLTPFVEENLVSAAGGSISHQVSFSYFNAFNSLLNNMELVRK
SLC25A13 Hs GRVTAIDFRDIMVTIRPHVLTPEECLVAAAGTTSHQVSFSYFNGFNSSLNNMELIRK

aralar1 Dm VYLHATEGSRTDMITKDQILLAAQTMQITPLEIDILFHLAGAVHQAGRIDYSDLSNIAP
SLC25A12 Hs IYSTLAGTRKDVEVTKEEFAQSAIRYGVQVTPLEIDILQLADLYNASGRLLADIERIAP
SLC25A13 Hs IYSTLAGTRKDVEVTKEEFVLAQQKFGQVTPMEVDILFQLADLYEPRGRMTLADIERIAP

aralar1 Dm EHYTKHMTHRLAEIKAVESPA--DRSAFIQVLESSYRFTLGSFAGAVGATVVYPIDLVKT
SLC25A12 Hs LAEG-ALPYNLAEQRRQSPG-LGRPIWLQIAESAYRFTLGSVAGAVGATAVYPIDLVKT
SLC25A13 Hs LEEG-TLPFNLAEEAQRKASGDSARPVLLQVAESAYRFGLGSVAGAVGATAVYPIDLVKT

aralar1 Dm RMQNQR-AGSYIGEVAYRNSWDCFKKVRHEGMGLYRGLLPQLMGVAPEKAIKLTVNDF
SLC25A12 Hs RMQNQRGSGSVVGEMLMYKNSFDCFKKVRHEGMGLYRGLLPQLIGVAPEKAIKLTVNDF
SLC25A13 Hs RMQNQRSTGSFVGELMYKNSFDCFKKVRHEGMGLYRGLLPQLLGVAPEKAIKLTVNDF

aralar1 Dm VRDKLTDKGNIPPTWAEVLAGGCAGASQVVFNTNPLEIVKIRLQVAGEIASGSKIRAWSVV
SLC25A12 Hs VRDKFRRDGSVPLPAEVLAGGCAGGSQVIFTNPLEIVKIRLQVAGEITTGPRVSALNVL
SLC25A13 Hs VRDKFMHKDGSPVLAEEILAGGCAGGSQVIFTNPLEIVKIRLQVAGEITTGPRVSALSVV

aralar1 Dm RELGLFGLYKGARACLLRDVPFSAIYFPTYAHTKAMMADKGYNHPLTLLAAGAIAGVPA
SLC25A12 Hs RDLGIFGLYKGAKACFLRDIPFSAIYFPCVYAHCKLLLADENGHVGGLNLLAAGAMAGVPA
SLC25A13 Hs RDLGFFGIYKGAKACFLRDIPFSAIYFPCVYAHVKASFANEDGQVSPGSLLLAGAIAGMPA

aralar1 Dm ASLVT PADVIKTRLQVVARSGQTTYGWWDATKKIMAEEGPRAFWKGTAARVFRSSPQFG
SLC25A12 Hs ASLVT PADVIKTRLQVAARAGQTTYSV рид CFRKILREEGPSAFWKGTAARVFRSSPQFG
SLC25A13 Hs ASLVT PADVIKTRLQVAARAGQTTYSV рид CFRKILREEGPKALWKGAGARVFRSSPQFG

aralar1 Dm VTLVTYELLQRLFYVDFGGTOPKGSEAHKITTPLEQAAASVTENVDHIGGYRAAVPLLA
SLC25A12 Hs VTLVTYELLQRFYIDFGGLKPAGSEP----TPKSRIAD-LPPANPDHIGGYRLATATFA
SLC25A13 Hs VTLVTYELLQRFYIDFGGVKPMGSEP----VPKSRIIN--LPAPNPDHVGGYKLAVATFA

aralar1 Dm GVESKFGYLPRFGRGVTAASPSTATGS---
SLC25A12 Hs GIENKFGLYLPKFKSPSVAVVQPKAAVAATQ
SLC25A13 Hs GIENKFGLYLPFK-PSVSTSKAIGGGP---

Figure 8. Expression of *aralar 1* Homologs in Mammalian Tissues

Figure 8A. Real-time PCR analysis of Slc25a12 expression in wild type mouse tissues (DCt Pancreas = 18,94)

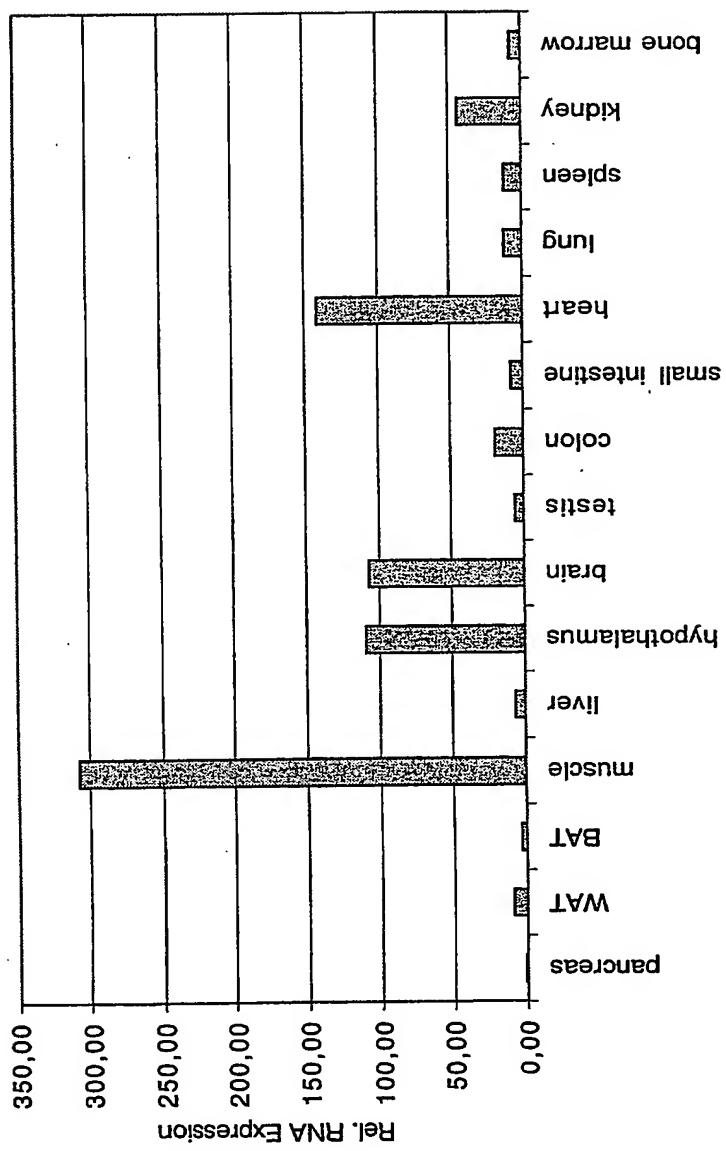


Figure 8B. Real-time PCR analysis of Slc25a12 expression in different mouse models

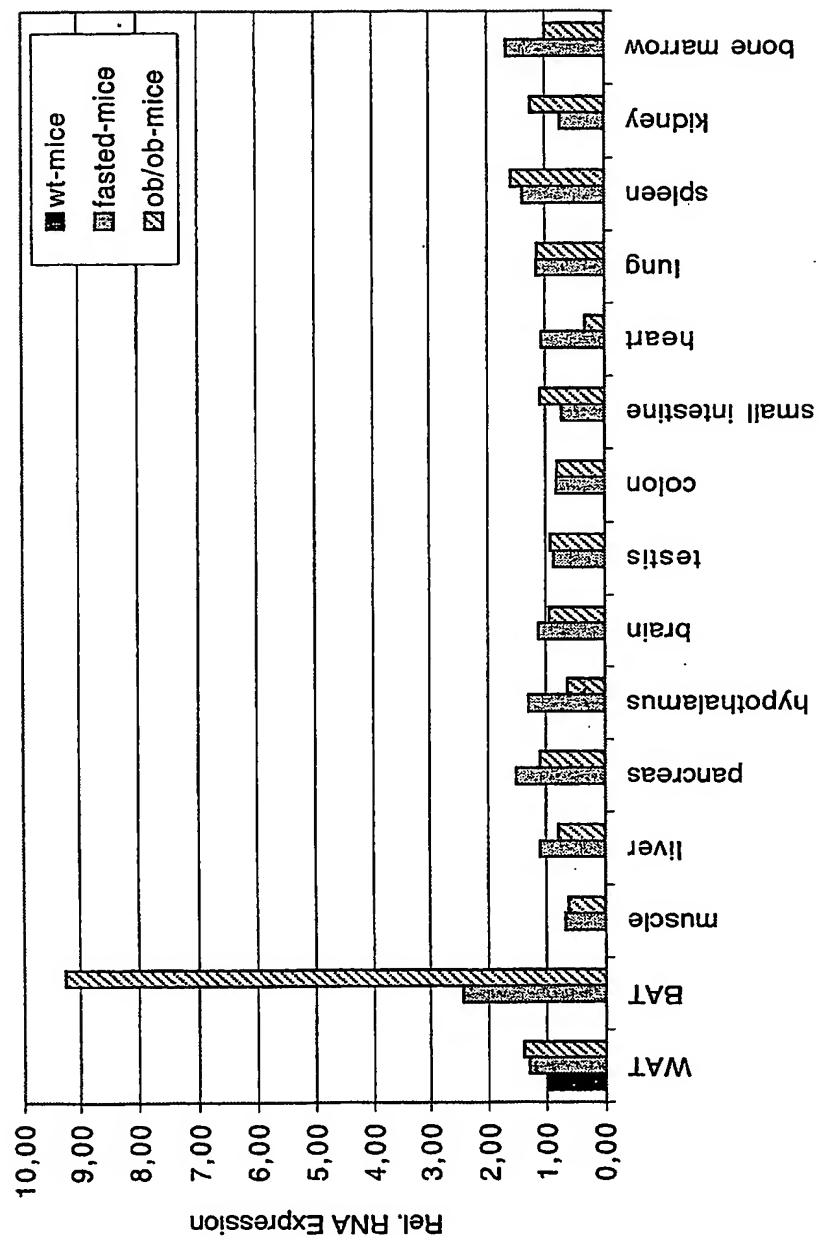


Figure 8C. Real-time PCR analysis of Slc25a13 expression in wild type mouse tissues (ΔCt Pancreas = 20,41)

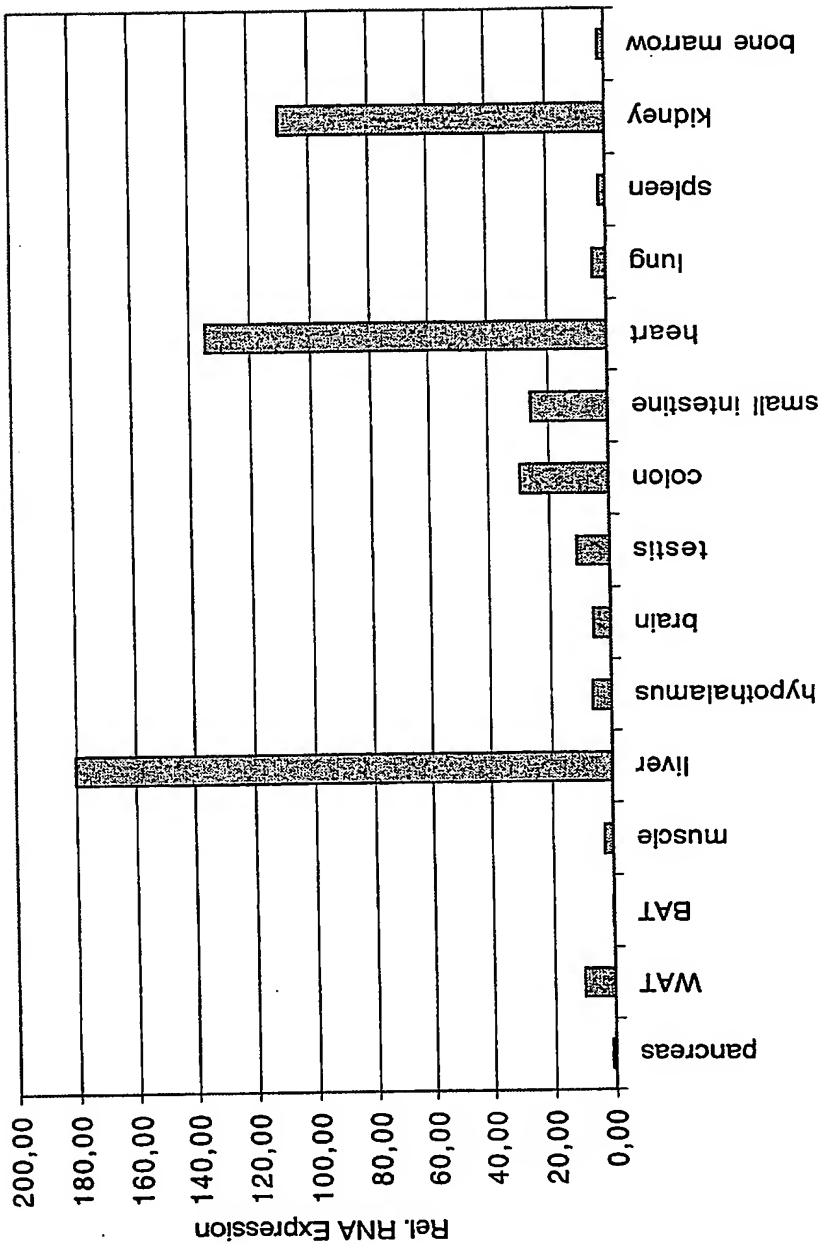


Figure 8D. Real-time PCR analysis of Slc25a13 expression in different mouse models

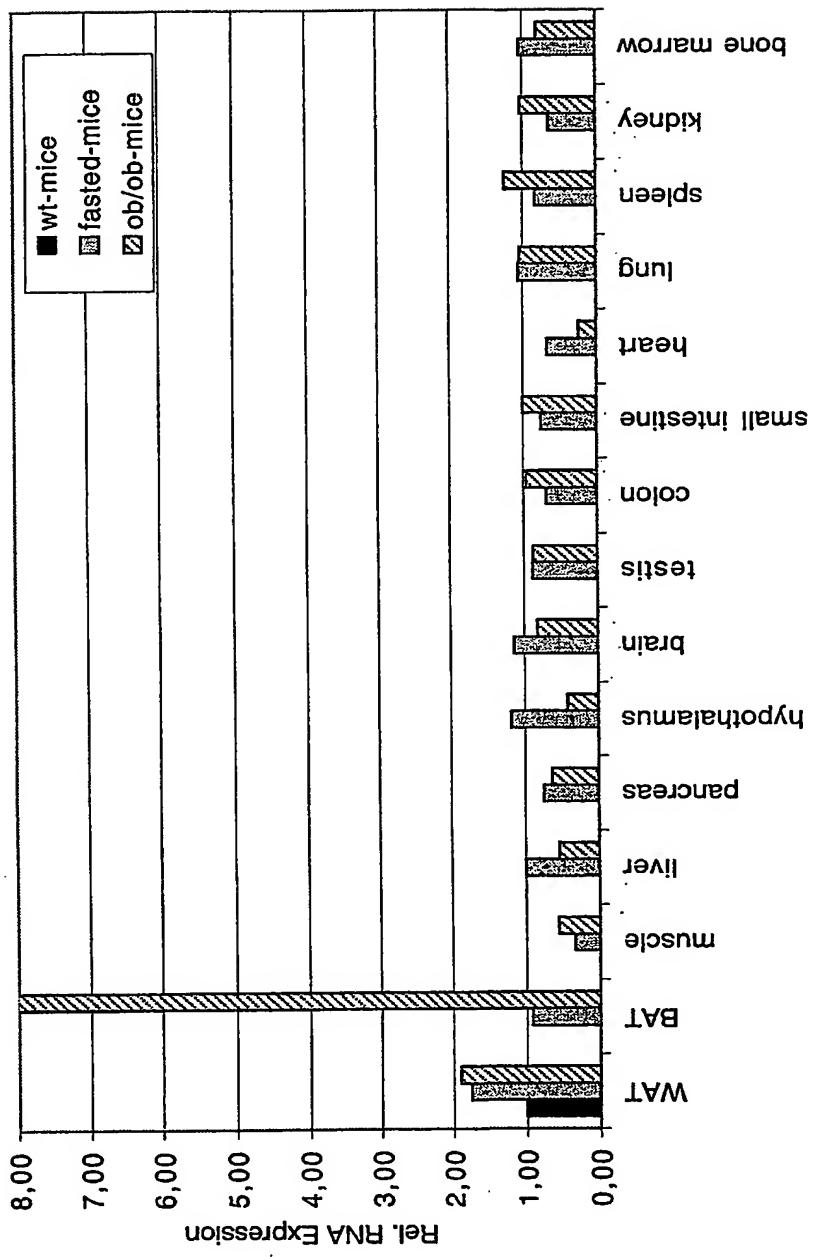


Figure 9. Triglyceride content of a *Drosophila how* (GadFly Accession Number CG10293) mutant

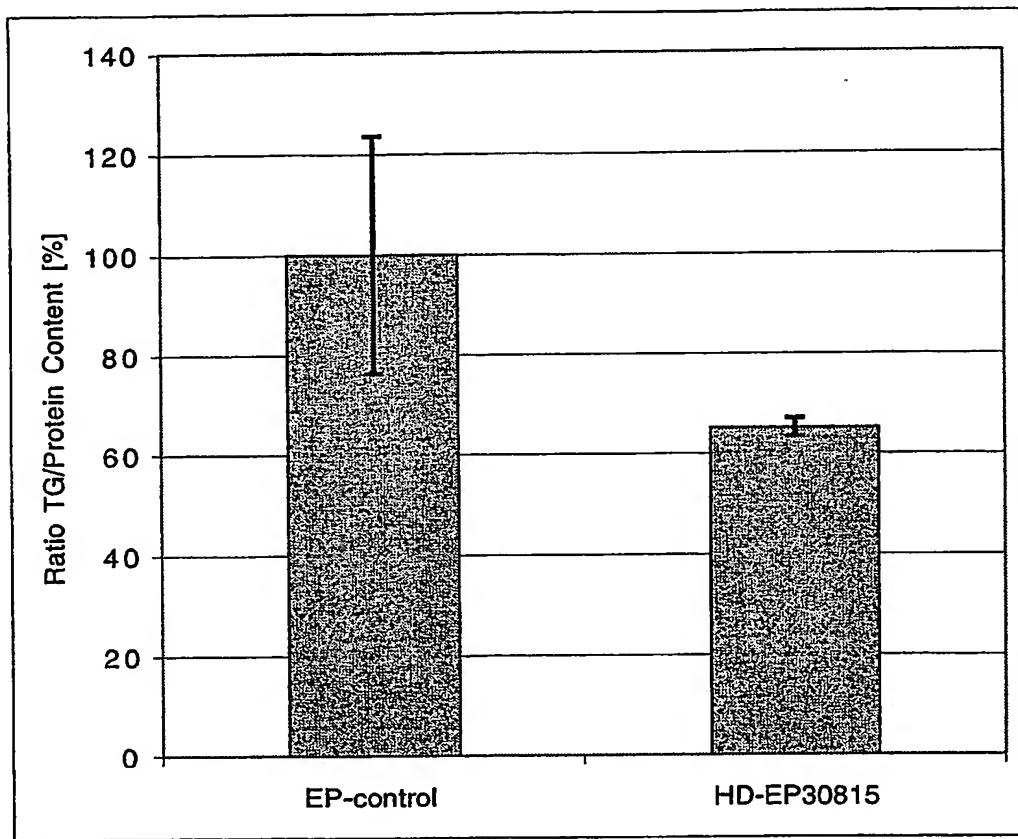


Figure 10. Molecular organisation of the *how* gene (GadFly Accession Number CG10293)

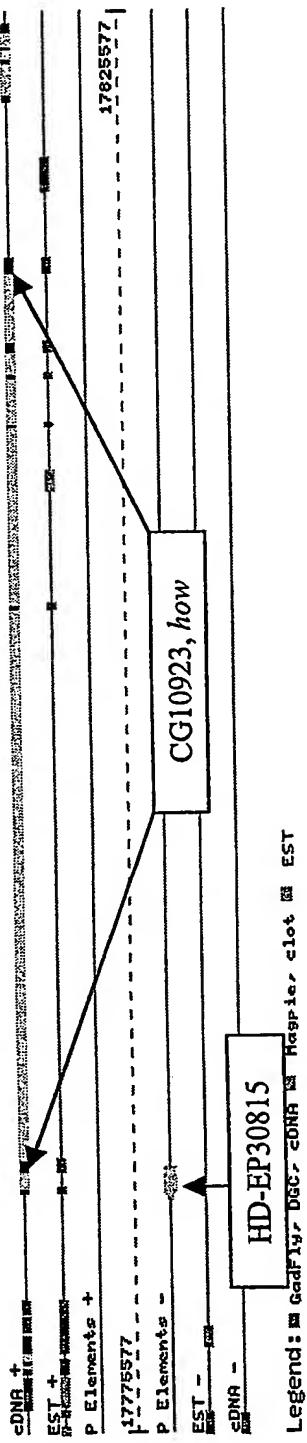


Figure 11. Homology of Drosopila *how* (GadFly Accession Number CG10293) to human Quaking isoforms

Figure 11A. BLASTP results for CG10293 (GadFly Accession Number)

gb|AAF63416.1|AF142421_1 (AF142421) QUAKING isoform 5 [Homo sapiens]
Length = 337

Score = 289 bits (739), Expect = 5e-77
Identities = 168/334 (50%), Positives = 215/334 (64%), Gaps = 20/334 (5%)
Query: 67 QQQQSTQSIADYLAQLLKDRKQLAAFPN---VFTHVERLLDEEIARVRASLFQ--ING-V 120
+ ++ + DYL QL+ D+K +++ PN +F H+ERLLDEEI+RVR ++ +NG
Sbjct: 2 ETKEKPKPPTPDYLMQLMNDKKLMSSLPNFCGIFNHLERLLDEEISRVRKDMYNDTLNGST 61
Query: 121 KKEPLTLPPEPEGSVVTMNEKVVVPVREHPDFNFVGRILGPRGMTAKOLEQETGCKIMVRG 180
+K LP+ G +V + EK+YVPV+E+PDFNFVGRILGPRG+TAKOLE ETGCKIMVRG
Sbjct: 62 EKRSAEELPAVGPIVQLQEKLVYVPVKEYPDFNFVGRILGPRGLTAKOLEAETGCKIMVRG 121
Query: 181 KGSMRDKKEDANRGKPWEHLSDDLHVLTVEDTENRATVKLAQAVAEVQKLLVPQAEG 240
KGSMRDKKKE+ NRGKPWEHL++DLHVLTVED +NRA +KL +AV EV+KLLVP AEG
Sbjct: 122 KGSMRDKKKEQNRGKPWEHLDHVLTVEDAQNRAEIKLKRAVEEVKKLLVPAAEG 181
Query: 241 EDELKKRQLMELAIINGTYRDTTAKSVAVCDEEWRRLVAASDSRLLTSTGLPGLAAQIRA 300
ED LKK QLMELAI+NGTYRD KS A+ A + R++T A +R
Sbjct: 182 EDSSLKKMQLMELAILNGTYRDNANKSPALAFS--LAATAQAAPRIITGPAPVLPPAALRT 239
Query: 301 PA-AAPLGAPLILNPRMTVPTTAASILSAQAAPTAAFDQQTG--HGMIFAPYDYANYAALA 357
P A P PLI + V + + PTAA G G+I+ PY+Y Y
Sbjct: 240 PTPAGPTIMPLIRQIQTAV-----MPNGTPHPTAAIVPPGPEAGLIYTPYEYP-YTLAP 292
Query: 358 GNPLLTEYADHS--VGAIKQQRRLATNREHPYQR 389
+L + S +GA+ + R R HPYQR
Sbjct: 293 ATSILEYPIEPSGVLGAVATKVRRHDMRVHPYQR 326

ref|XP_037438.2| (XM_037438) similar to KH domain RNA binding protein QKI-5A [Homo sapiens], Length = 341

Score = 289 bits (739), Expect = 5e-77
Identities = 168/334 (50%), Positives = 215/334 (64%), Gaps = 20/334 (5%)
Query: 67 QQQQSTQSIADYLAQLLKDRKQLAAFPN---VFTHVERLLDEEIARVRASLFQ--ING-V 120
+ ++ + DYL QL+ D+K +++ PN +F H+ERLLDEEI+RVR ++ +NG
Sbjct: 6 ETKEKPKPPTPDYLMQLMNDKKLMSSLPNFCGIFNHLERLLDEEISRVRKDMYNDTLNGST 65
Query: 121 KKEPLTLPPEPEGSVVTMNEKVVVPVREHPDFNFVGRILGPRGMTAKOLEQETGCKIMVRG 180
+K LP+ G +V + EK+YVPV+E+PDFNFVGRILGPRG+TAKOLE ETGCKIMVRG
Sbjct: 66 EKRSAEELPAVGPIVQLQEKLVYVPVKEYPDFNFVGRILGPRGLTAKOLEAETGCKIMVRG 125
Query: 181 KGSMRDKKEDANRGKPWEHLSDDLHVLTVEDTENRATVKLAQAVAEVQKLLVPQAEG 240
KGSMRDKKKE+ NRGKPWEHL++DLHVLTVED +NRA +KL +AV EV+KLLVP AEG
Sbjct: 126 KGSMRDKKKEQNRGKPWEHLDHVLTVEDAQNRAEIKLKRAVEEVKKLLVPAAEG 185
Query: 241 EDELKKRQLMELAIINGTYRDTTAKSVAVCDEEWRRLVAASDSRLLTSTGLPGLAAQIRA 300
ED LKK QLMELAI+NGTYRD KS A+ A + R++T A +R
Sbjct: 186 EDSSLKKMQLMELAILNGTYRDNANKSPALAFS--LAATAQAAPRIITGPAPVLPPAALRT 243

Query: 301 PA-AAPLGAPLILNPRMTVPTTAASILSAQAAPTAAFDQTG--HGMIFAPYDYANYAALA 357
 P A P PLI + V + + PTAA G G+I+ PY+Y Y
 Sbjct: 244 PTPAGPTIMPLIRQIQTAV-----MPNGTPHPTAAIVPPGPEAGLIYTPYEYP-YTLAP 296

Query: 358 GNPLLTEYADHS--VGAIKQQRRLATNREHPYQR 389
 +L + S +GA+ + R R HPYQR
 Sbjct: 297 ATSILEYPIEPSGVGLGAVATKVRHDMRVHPYQR 330

gb|AAF63414.1|AF142419_1 (AF142419) QUAKING isoform 6 [Homo sapiens]
 Length = 363

Score = 289 bits (739), Expect = 5e-77
 Identities = 168/334 (50%), Positives = 215/334 (64%), Gaps = 20/334 (5%)

Query: 67 QQQQSTQSIADYLAQLLKDRKQLAAFPN---VFTHVERLLDEEIARVRASLFQ--ING-V 120
 + ++ + DYL QL+ D+K +++ PN +F H+ERLLDEEI+RVR ++ +NG
 Sbjct: 28 ETKEPKPKPTPDYLMQLMNDKKLMSLPNFCGIFNHLERLLDEEISRVRKDMYNDTLNGST 87

Query: 121 KKEPLTLPPEPEGSVVTMNEKVYVPVREHPDFNFVGRILGPRGMTAKQLEQETGCKIMVRG 180
 +K LP+ G +V + EK+YVPV+E+PDFNFVGRILGPRG+TAKQLE ETGCKIMVRG
 Sbjct: 88 EKRSAAELPDAVGPIVQLQEKLVYVPKEYPDFNFVGRILGPRGLTAKQLEAETGCKIMVRG 147

Query: 181 KGSMRDKKEDANRGKPWEHLSDLHVLTITVEDTENRATVKLAQAVAEVQKLLVPQAEG 240
 KGSMRDKKKE+ NRGKPWEHL++DLHVLTITVED +NRA +KL +AV EV+KLLVP AEG
 Sbjct: 148 KGSMRDKKKEQNRGKPWEHLNEDLHVLTITVEDAQNRAEIKLKRAVEEVKLLVPAAEG 207

Query: 241 EDELKKRQLMELAIINGTYRDTTAKSVAVCDEEWRLVAASDSRLLTSTGLPGLAAQIRA 300
 ED LKK QLMELAI+NGTYRD KS A+ A + R++T A +R
 Sbjct: 208 EDSLKKMQLMELAILNGTYRDANIKSPALAFS--LAATAQAAPRIITGPAPVLPPAALRT 265

Query: 301 PA-AAPLGAPLILNPRMTVPTTAASILSAQAAPTAAFDQTG--HGMIFAPYDYANYAALA 357
 P A P PLI + V + + PTAA G G+I+ PY+Y Y
 Sbjct: 266 PTPAGPTIMPLIRQIQTAV-----MPNGTPHPTAAIVPPGPEAGLIYTPYEYP-YTLAP 318

Query: 358 GNPLLTEYADHS--VGAIKQQRRLATNREHPYQR 389
 +L + S +GA+ + R R HPYQR
 Sbjct: 319 ATSILEYPIEPSGVGLGAVATKVRHDMRVHPYQR 352

dbj|BAB55032.1| (AK027309) unnamed protein product [Homo sapiens]
 Length = 323

Score = 282 bits (722), Expect = 5e-75
 Identities = 165/320 (51%), Positives = 208/320 (64%), Gaps = 20/320 (6%)

Query: 81 QLKDRKQLAAFPN---VFTHVERLLDEEIARVRASLFQ--ING-VKKEPLTLPPEPEGSV 134
 QL+ D+K +++ PN +F H+ERLLDEEI+RVR ++ +NG +K LP+ G +
 Sbjct: 2 QLMNDKKLMSLPNFCGIFNHLERLLDEEISRVRKDMYNDTLNGSTEKRSAELPDAVGPI 61

Query: 135 VTMNEKVYVPVREHPDFNFVGRILGPRGMTAKQLEQETGCKIMVRGKGSMRDKKEDANR 194
 V + EK+YVPV+E+PDFNFVGRILGPRG+TAKQLE ETGCKIMVRGKGSMRDKKKE+ NR
 Sbjct: 62 VQLQEKLVYVPKEYPDFNFVGRILGPRGLTAKQLEAETGCKIMVRGKGSMRDKKKEQNR 121

Query: 195 GKPWEHLSDLHVLTITVEDTENRATVKLAQAVAEVQKLLVPQAEGEDELKKRQLMELAI 254
 GKPWEHL++DLHVLTITVED +NRA +KL +AV EV+KLLVP AEGED LKK QLMELAI
 Sbjct: 122 GKPWEHLNEDLHVLTITVEDAQNRAEIKLKRAVEEVKLLVPAAEGEDSLKKMQLMELAI 181

Query: 255 INGTYRDTTAKSVAVCDEEWRLVAASDSRLLTGLPGLAAQIRAPA-AAPLGAPLILN 313
 +NGTYRD KS A+ A + R++T A +R P A P PLI
 Sbjct: 182 LNGTYRDNANKSPALAFS--LAATAQAAPRIITGPAPVLPPAALRTPTPAGPTIMPLIRQ 239

Query: 314 PRMTVPTTAASILSAQAAPTAADFQTG--HGMIFAPYDYANYAALAGNPLLTEYADHS-- 369
 + V + + PTAA G G+I+ PY+Y Y +L + S
 Sbjct: 240 IQTAV-----MPNGTPHPTAAIVPPGPEAGLIYTPYEYP-YTLAPATSILEYPIEPSGV 292

Query: 370 VGAIIKQQRRLATNREHPYQR 389
 +GA+ + R R HPYQR
 Sbjct: 293 LGAVATKVRRHDMRVHPYQR 312

gb|AAF63413.1|AF142418_1 (AF142418) QUAKing isoform 2 [Homo sapiens]
 Length = 347

Score = 280 bits (716), Expect = 2e-74
 Identities = 156/293 (53%), Positives = 198/293 (67%), Gaps = 17/293 (5%)

Query: 67 QQQQSTQSIADYLAQLLKDRKQLAAFPN---VFTHVERLLDEEIARVRASLFQ--ING-V 120
 + ++ + DYL QL+ D+K +++ PN +F H+ERLLDEEI+RVR ++ +NG
 Sbjct: 28 ETKEKPKPPTPDYLMQLMNDKKLMSSLNFCCGIFNHLERLLDEEISVRKDMYNDTLNGST 87

Query: 121 KKEPLTLPEPEGSVVTMNEKVYVPVREHPDFNFVGRILGPRGMTAKQLEQETGCKIMVRG 180
 +K LP+ G +V + EK+YVPV+E+PDFNFVGRILGPRG+TAKQLE ETGCKIMVRG
 Sbjct: 88 EKRSAEELPDAVGPIVQLQEKLIVPVKEYPDFNFVGRILGPRGLTAKQLEAETGCKIMVRG 147

Query: 181 KGSMRDKKEDANRGKPWEHLSDDLHVLITVEDTENRATVKLAQAVAEVQKLLVPQAEG 240
 KGSMRDKKKE+ NRGKPWEHL++DLHVLITVED +NRA +KL +AV EV+KLLVP AEG
 Sbjct: 148 KGSMRDKKKEQNRGKPWEHLDLHVLITVEDAQNRAEIKLKRAVEEVKKLLVPAAEG 207

Query: 241 EDELKKRQLMELAIINGTYRDTTAKSVAVCDEEWRLVAASDSRLLTGLPGLAAQIRA 300
 ED LKK QLMELAI+NGTYRD KS A+ A + R++T A +R
 Sbjct: 208 EDSDLKKMQLMELAILNGTYRDNANKSPALAFS--LAATAQAAPRIITGPAPVLPPAALRT 265

Query: 301 PA-AAPLGAPLILNPRMTVPTTAASILSAQAAPTAADFQTG--HGMIFAPYDY 350
 P A P PLI + V + + PTAA G G+I+ PY+Y
 Sbjct: 266 PTPAGPTIMPLIRQIQTAV-----MPNGTPHPTAAIVPPGPEAGLIYTPYEY 312

gb|AAF63417.1|AF142422_1 (AF142422) QUAKing isoform 3 [Homo sapiens]
 Length = 341

Score = 280 bits (716), Expect = 2e-74
 Identities = 156/293 (53%), Positives = 198/293 (67%), Gaps = 17/293 (5%)

Query: 67 QQQQSTQSIADYLAQLLKDRKQLAAFPN---VFTHVERLLDEEIARVRASLFQ--ING-V 120
 + ++ + DYL QL+ D+K +++ PN +F H+ERLLDEEI+RVR ++ +NG
 Sbjct: 28 ETKEKPKPPTPDYLMQLMNDKKLMSSLNFCCGIFNHLERLLDEEISVRKDMYNDTLNGST 87

Query: 121 KKEPLTLPEPEGSVVTMNEKVYVPVREHPDFNFVGRILGPRGMTAKQLEQETGCKIMVRG 180
 +K LP+ G +V + EK+YVPV+E+PDFNFVGRILGPRG+TAKQLE ETGCKIMVRG
 Sbjct: 88 EKRSAEELPDAVGPIVQLQEKLIVPVKEYPDFNFVGRILGPRGLTAKQLEAETGCKIMVRG 147

Query: 181 KGSMRDKKEDANRGKPWEHLSDDLHVLITVEDTENRATVKLAQAVAEVQKLLVPQAEG 240
 KGSMRDKKKE+ NRGKPWEHL++DLHVLITVED +NRA +KL +AV EV+KLLVP AEG
 Sbjct: 148 KGSMRDKKKEQNRGKPWEHLDLHVLITVEDAQNRAEIKLKRAVEEVKKLLVPAAEG 207

Query: 241 EDELKKRQLMELAIINGTYRDTTAKSVAVCDEEWRLVAASDSRLLTSTGLPGLAAQIRA 300
 ED LKK QLMELAI+NGTYRD KS A+ A + R++T A +R
 Sbjct: 208 EDSLKKMQLMELAILNGTYRDANIKSPALAFS--LAATAQAAPRIITGPAPVLPPAALRT 265

Query: 301 PA-AAPLGAPLILNPRMTVPTTAASILSAQAAAPTAAFDQTG--HGMIFAPYDY 350
 P A P PLI + V + + PTAA G G+I+ PY+Y
 Sbjct: 266 PTPAGPTIMPLIRQIQTAV-----MPNGTPHPTAAIVPPGPEAGLIYTPYEY 312

gb|AAF63415.1|AF142420_1 (AF142420) QUAKING isoform 4 [Homo sapiens]
 Length = 315

Score = 280 bits (716), Expect = 2e-74
 Identities = 156/293 (53%), Positives = 198/293 (67%), Gaps = 17/293 (5%)

Query: 67 QQQQSTQSIADYLAQLLKDRKQLAAFPN---VFTHVERLLDEEIARVRASLFQ--ING-V 120
 + ++ + DYL QL+ D+K +++ PN +F H+ERLLDEEI+RVR ++ +NG
 Sbjct: 2 ETKEKPCKPTPDYLMQLMNDKLMSSLNPFCGIFNHLERLLDEEISVRKDMYNDTLNGST 61

Query: 121 KKEPLTLPEPEGSVVTMNEKVVVPVREHPDFNFVGRILGPRGMTAKQLEQETGCKIMVRG 180
 +K LP+ G +V + EK+YVPV+E+PDFNFVGRILGPRG+TAKQLE ETGCKIMVRG
 Sbjct: 62 EKRSAELPDAVGPIVQLQEKLIVPVKEYPDFNFVGRILGPRGLTAKQLEAETGCKIMVRG 121

Query: 181 KGSMRDKKKEDANRGKPWEHLSDDLHVLITVEDTENRATVKLAQAVAEVQKLLVPQAEG 240
 KGSMRDKKK+ NRGKPWEHL++DLHVLITVED +NRA +KL +AV EV+KLLVP AEG
 Sbjct: 122 KGSMRDKKKEEQRGKPWEHLDLHVLITVEDAQNRRAEIKLKRAVEEVKLLVPAAEG 181

Query: 241 EDELKKRQLMELAIINGTYRDTTAKSVAVCDEEWRLVAASDSRLLTSTGLPGLAAQIRA 300
 ED LKK QLMELAI+NGTYRD KS A+ A + R++T A +R
 Sbjct: 182 EDSLKKMQLMELAILNGTYRDANIKSPALAFS--LAATAQAAPRIITGPAPVLPPAALRT 239

Query: 301 PA-AAPLGAPLILNPRMTVPTTAASILSAQAAAPTAAFDQTG--HGMIFAPYDY 350
 P A P PLI + V + + PTAA G G+I+ PY+Y
 Sbjct: 240 PTPAGPTIMPLIRQIQTAV-----MPNGTPHPTAAIVPPGPEAGLIYTPYEY 286

dbj|BAB69497.1| (AB067799) RNA binding protein HQK-6 [Homo sapiens]
 Length = 319

Score = 280 bits (716), Expect = 2e-74
 Identities = 156/293 (53%), Positives = 198/293 (67%), Gaps = 17/293 (5%)

Query: 67 QQQQSTQSIADYLAQLLKDRKQLAAFPN---VFTHVERLLDEEIARVRASLFQ--ING-V 120
 + ++ + DYL QL+ D+K +++ PN +F H+ERLLDEEI+RVR ++ +NG
 Sbjct: 6 ETKEKPCKPTPDYLMQLMNDKLMSSLNPFCGIFNHLERLLDEEISVRKDMYNDTLNGST 65

Query: 121 KKEPLTLPEPEGSVVTMNEKVVVPVREHPDFNFVGRILGPRGMTAKQLEQETGCKIMVRG 180
 +K LP+ G +V + EK+YVPV+E+PDFNFVGRILGPRG+TAKQLE ETGCKIMVRG
 Sbjct: 66 EKRSAELPDAVGPIVQLQEKLIVPVKEYPDFNFVGRILGPRGLTAKQLEAETGCKIMVRG 125

Query: 181 KGSMRDKKKEDANRGKPWEHLSDDLHVLITVEDTENRATVKLAQAVAEVQKLLVPQAEG 240
 KGSMRDKKK+ NRGKPWEHL++DLHVLITVED +NRA +KL +AV EV+KLLVP AEG
 Sbjct: 126 KGSMRDKKKEEQRGKPWEHLDLHVLITVEDAQNRRAEIKLKRAVEEVKLLVPAAEG 185

Query: 241 EDELKKRQLMELAIINGTYRDTTAKSVAVCDEEWRLVAASDSRLLTSTGLPGLAAQIRA 300
 ED LKK QLMELAI+NGTYRD KS A+ A + R++T A +R
 Sbjct: 186 EDSLKKMQLMELAILNGTYRDANIKSPALAFS--LAATAQAAPRIITGPAPVLPPAALRT 243

Query: 301 PA-AAPLGAPILILNPRMTVPTTAASILSAQAAAPTAAFDQTG--HGMIFAPYDY 350
 P A P PLI + V + + PTAA G G+I+ PY+Y
 Sbjct: 244 PTPAGPTIMPLIRQIQTAV-----MPNGTPHPTAAIVPPGPEAGLIYTPYEY 290

dbj|BAB69499.1| (AB067801) RNA binding protein HQK-7B [Homo sapiens]
 Length = 319

Score = 280 bits (716), Expect = 2e-74
 Identities = 156/293 (53%), Positives = 198/293 (67%), Gaps = 17/293 (5%)

Query: 67 QQQQSTQSIADYLAQLLKDRKQLAAFPN---VFTHVERLLDEEIARVRASLFQ--ING-V 120
 + ++ + DYL QL+ D+K +++ PN +F H+ERLLDEEI+RVR ++ +NG
 Sbjct: 6 ETKEKPCKPTPDYLMQLMNDKKLMSLPNFCGIFNHLLDEEISRVRKDMYNDTLNGST 65

Query: 121 KKEPLTLPPEPEGSVVTMNEKVYVPVREHPDFNFVGRILGPRGMTAKQLEQETGCKIMVRG 180
 +K LP+ G +V + EK+YVPV+E+PDFNFVGRILGPRG+TAKQLE ETGCKIMVRG
 Sbjct: 66 EKRSAAELPDAVGPIVQLQEKLIVPVKEYPDFNFVGRILGPRGLTAKQLEAETGCKIMVRG 125

Query: 181 KGSMRDKKKEDANRGKPWEHLSDLHVLTVEDTENRATVKLAQAVAEVQKLLVPQAEG 240
 KGSMRDKKKE+ NRGKPWEHL++DLHVLTVED +NRA +KL +AV EV+KLLVP AEG
 Sbjct: 126 KGSMRDKKKEEQNRGKPWEHLNEDLHVLTVEDAQNRAEIKLKRRAVEEVKLLVPAAEG 185

Query: 241 EDELKKRQLMELAIINGTYRDTTAKSVAVCDEEWRLVAASDSRLLTGLPGLAAQIRA 300
 ED LKK QLMELAI+NGTYRD KS A+ A + R++T A +R
 Sbjct: 186 EDSLKKMQLMELAILNGTYRDANIKSPALAFS--LAATAQAAPRIITGPAPVLPPAALRT 243

Query: 301 PA-AAPLGAPILILNPRMTVPTTAASILSAQAAAPTAAFDQTG--HGMIFAPYDY 350
 P A P PLI + V + + PTAA G G+I+ PY+Y
 Sbjct: 244 PTPAGPTIMPLIRQIQTAV-----MPNGTPHPTAAIVPPGPEAGLIYTPYEY 290

dbj|BAB69498.1| (AB067800) RNA binding protein HQK-7 [Homo sapiens]
 Length = 325

Score = 280 bits (716), Expect = 2e-74
 Identities = 156/293 (53%), Positives = 198/293 (67%), Gaps = 17/293 (5%)

Query: 67 QQQQSTQSIADYLAQLLKDRKQLAAFPN---VFTHVERLLDEEIARVRASLFQ--ING-V 120
 + ++ + DYL QL+ D+K +++ PN +F H+ERLLDEEI+RVR ++ +NG
 Sbjct: 6 ETKEKPCKPTPDYLMQLMNDKKLMSLPNFCGIFNHLLDEEISRVRKDMYNDTLNGST 65

Query: 121 KKEPLTLPPEPEGSVVTMNEKVYVPVREHPDFNFVGRILGPRGMTAKQLEQETGCKIMVRG 180
 +K LP+ G +V + EK+YVPV+E+PDFNFVGRILGPRG+TAKQLE ETGCKIMVRG
 Sbjct: 66 EKRSAAELPDAVGPIVQLQEKLIVPVKEYPDFNFVGRILGPRGLTAKQLEAETGCKIMVRG 125

Query: 181 KGSMRDKKKEDANRGKPWEHLSDLHVLTVEDTENRATVKLAQAVAEVQKLLVPQAEG 240
 KGSMRDKKKE+ NRGKPWEHL++DLHVLTVED +NRA +KL +AV EV+KLLVP AEG
 Sbjct: 126 KGSMRDKKKEEQNRGKPWEHLNEDLHVLTVEDAQNRAEIKLKRRAVEEVKLLVPAAEG 185

Query: 241 EDELKKRQLMELAIINGTYRDTTAKSVAVCDEEWRLVAASDSRLLTGLPGLAAQIRA 300
 ED LKK QLMELAI+NGTYRD KS A+ A + R++T A +R
 Sbjct: 186 EDSLKKMQLMELAILNGTYRDANIKSPALAFS--LAATAQAAPRIITGPAPVLPPAALRT 243

Query: 301 PA-AAPLGAPILILNPRMTVPTTAASILSAQAAAPTAAFDQTG--HGMIFAPYDY 350
 P A P PLI + V + + PTAA G G+I+ PY+Y
 Sbjct: 244 PTPAGPTIMPLIRQIQTAV-----MPNGTPHPTAAIVPPGPEAGLIYTPYEY 290

gb|AAF63412.1|AF142417_1 (AF142417) QUAKING isoform 1 [Homo sapiens]
Length = 321

Score = 280 bits (716), Expect = 2e-74
Identities = 156/293 (53%), Positives = 198/293 (67%), Gaps = 17/293 (5%)

Query: 67 QQQQSTQSIADYLAQLLKDRKQLAAFPN---VFTHVERLLDEEIARVRASLFQ--ING-V 120
+ ++ + DYL QL+ D+K +++ PN +F H+ERLLDEEI+RVR ++ +NG
Sbjct: 2 ETKEKPKPPTPDYLMQLMNDKKLMSSLPNFCGIFNHLERLLDEEISRVRKDMYNDTLNGST 61

Query: 121 KKEPLTLPEPEGSVVTMNEKVYVPVREHPDFNFVGRILGPRGMTAKQLEQETGCKIMVRG 180
+K LP+ G +V + EK+YVPV+E+PDFNFVGRILGPRG+TAKQLE ETGCKIMVRG
Sbjct: 62 EKRSAAELPDAVGPIVQLQEKLKYVPVKEYPDFNFVGRILGPRGLTAKQLEAETGCKIMVRG 121

Query: 181 KGSMRDKKEDANRGKPNWEHLSDLHVLLITVEDTENRATVKLAQAVAEVQKLLVPQAEG 240
KGSMRDKKKE+ NRGKPNWEHL++DLHVLLITVED +NRA +KL +AV EV+KLLVP AEG
Sbjct: 122 KGSMRDKKKEQNRGKPNWEHLNEDLVLLITVEDAQNRRAEIKLKRAVEEVKKLLVPAAEG 181

Query: 241 EDELKKRQLMELAIINGTYRDTTAKSVAVCDEEWRLVAASDSRLLTSTGLPGLAAQIRA 300
ED LKK QLMELAI+NGTYRD KS A+ A + R++T A +R
Sbjct: 182 EDSLKKMQLMELAILNGTYRDNIAKSPALAFS--LAATAQAAPRIITGPAPVLPPAALRT 239

Query: 301 PA-AAPLGAPLILNPRMTVPTTAASILSAQAAPTAAFDQTG--HGMIFAPYDY 350
P A P PLI + V + + PTAA G G+I+ PY+Y
Sbjct: 240 PTPAGPTIMPLIRQIQTAV-----MPNGTPHPTAAIVPPGPEAGLIYTPYEY 286

dbj|BD004960.1| Genes related to stomach cancer, Length = 1993

Score = 288 bits (738), Expect = 1e-77
Identities = 168/324 (51%), Positives = 211/324 (64%), Gaps = 11/324 (3%)
Frame = +1

Query: 77 DYLAQLLKDRKQLAAFPN---VFTHVERLLDEEIARVRASLFQ--ING-VKKEPLTLPEP 130
DYL QL+ D+K +++ PN +F H+ERLLDEEI+RVR ++ +NG +K LP+
Sbjct: 4 DYLMQLMNDKKLMSSLPNFCGIFNHLERLLDEEISRVRKDMYNDTLNGSTEKRSAAELPDA 183

Query: 131 EGSSVVTMNEKVYVPVREHPDFNFVGRILGPRGMTAKQLEQETGCKIMVRGKGSMRDKKKE 190
G +V + EK+YVPV+E+PDFNFVGRILGPRG+TAKQLE ETGCKIMVRGKGSMRDKKKE
Sbjct: 184 VGPIVQLQEKLKYVPVKEYPDFNFVGRILGPRGLTAKQLEAETGCKIMVRGKGSMRDKKKE 363

Query: 191 DANRGKPNWEHLSDLHVLLITVEDTENRATVKLAQAVAEVQKLLVPQAEGEDELKKRQLM 250
+ NRGKPNWEHL++DLHVLLITVED +NRA +KL +AV EV+KLLVP AEGED LKK QLM
Sbjct: 364 EQNRGKPNWEHLNEDLVLLITVEDAQNRRAEIKLKRAVEEVKKLLVPAAEGEDSLKKMQLM 543

Query: 251 ELAIINGTYRDTTAKSVAVCDEEWRLVAASDSRLLTSTGLPGLAAQIRAPA-AAPLGAP 309
ELAI+NGTYRD KS A+ A + R++T A +R P A P P
Sbjct: 544 ELAIINGTYRDNIAKSPALAFS--LAATAQAAPRIITGPAPVLPPAALRTPTPAGPTIMP 717

Query: 310 LILNPRMTVPTTAASILSAQAAPTAAFDQTG--HGMIFAPYDYANYAALAGNPLLTEYAD 367
LI + V + + PTAA G G+I+ PY+Y Y +L +
Sbjct: 718 LIRQIQTAV-----MPNGTPHPTAAIVPPGPEAGLIYTPYEY-P-TLAPATSILEYPIE 876

Query: 368 HS--VGAIIKQQRRLATNREHPYQR 389
S +GA+ + R R HPYQR
Sbjct: 877 PSGVLGAVATKVRHRDMRVHPYQR

Figure 11B. Multiple Sequence Alignment (ClustalW 1.83)

CG10293 Dm MSVCESKAVVQQQLQOHLQQQAAAVVAVAQQQQAQAAQAAQAAQAAQQQQQAPQVVVPMT P
 QKI-6 Hs -----MLSLSSLRRNSGRNSGSCGAWN-----
 QKI-2 Hs -----MLSLSSLRRNSGRNSGSCGAWN-----
 QKI-3 Hs -----MLSLSSLRRNSGRNSGSCGAWN-----
 HQK-7B Hs -----

CG10293 Dm QHLTPQQQQQSTOSIADYLAQLLKDRKQLAAFPN---VFTHVERLLDEEIARVRASLF--
 QKI-6 Hs -MVGEMETKEPKPPTPDYLMQLMNDKKLMSSLNPFCGIFNHLERLLDEEIISVRKDMYND
 QKI-2 Hs -MVGEMETKEPKPPTPDYLMQLMNDKKLMSSLNPFCGIFNHLERLLDEEIISVRKDMYND
 QKI-3 Hs -MVGEMETKEPKPPTPDYLMQLMNDKKLMSSLNPFCGIFNHLERLLDEEIISVRKDMYND
 HQK-7B Hs -MVGEMETKEPKPPTPDYLMQLMNDKKLMSSLNPFCGIFNHLERLLDEEIISVRKDMYND

CG10293 Dm QING-VKKEPLTLPEPEGSVVTMNEKVYVPVREHPDFNFVGRILGPRGMTAKQLEQETGC
 QKI-6 Hs TLNGSTEKRSALPDAVGPIVQLQEKL YVPVKEYPDFNFVGRILGPRGLTAKQLEAETGC
 QKI-2 Hs TLNGSTEKRSALPDAVGPIVQLQEKL YVPVKEYPDFNFVGRILGPRGLTAKQLEAETGC
 QKI-3 Hs TLNGSTEKRSALPDAVGPIVQLQEKL YVPVKEYPDFNFVGRILGPRGLTAKQLEAETGC
 HQK-7B Hs TLNGSTEKRSALPDAVGPIVQLQEKL YVPVKEYPDFNFVGRILGPRGLTAKQLEAETGC

CG10293 Dm KIMVRGKGSMRDKKKEDANRGKPWEHLSDDLHVLITVEDTENRATVKLAQAVAEVQKLL
 QKI-6 Hs KIMVRGKGSMRDKKKEEQNRGKPWEHLNEDLHVLITVEDAQNRAEIKLKRAVEEVKKLL
 QKI-2 Hs KIMVRGKGSMRDKKKEEQNRGKPWEHLNEDLHVLITVEDAQNRAEIKLKRAVEEVKKLL
 QKI-3 Hs KIMVRGKGSMRDKKKEEQNRGKPWEHLNEDLHVLITVEDAQNRAEIKLKRAVEEVKKLL
 HQK-7B Hs KIMVRGKGSMRDKKKEEQNRGKPWEHLNEDLHVLITVEDAQNRAEIKLKRAVEEVKKLL

CG10293 Dm VPQAEGEDELKKRQLMELAIINGTYRDTTAKSVAVCDEEWRRLVAASDSRLLTSTGLPGL
 QKI-6 Hs VPAAEGEDSLKKMQLMELAILNGTYRDANIKSPALAFSLAATAQAAP--RIITGPAPVLP
 QKI-2 Hs VPAAEGEDSLKKMQLMELAILNGTYRDANIKSPALAFSLAATAQAAP--RIITGPAPVLP
 QKI-3 Hs VPAAEGEDSLKKMQLMELAILNGTYRDANIKSPALAFSLAATAQAAP--RIITGPAPVLP
 HQK-7B Hs VPAAEGEDSLKKMQLMELAILNGTYRDANIKSPALAFSLAATAQAAP--RIITGPAPVLP

CG10293 Dm AAQIRAP-AAAPLGAPLILNPRMTVPTTAASILSAQAAPTAADFQTG--HGMIFAPYDYA
 QKI-6 Hs PAALRTPTPAGPTIMPLIR-----QIQTAVMPNGTPHPTAAIVPPGPEAGLIYTPYEYP
 QKI-2 Hs PAALRTPTPAGPTIMPLIR-----QIQTAVMPNGTPHPTAAIVPPGPEAGLIYTPYEYP
 QKI-3 Hs PAALRTPTPAGPTIMPLIR-----QIQTAVMPNGTPHPTAAIVPPGPEAGLIYTPYEYP
 HQK-7B Hs PAALRTPTPAGPTIMPLIR-----QIQTAVMPNGTPHPTAAIVPPGPEAGLIYTPYEYP

CG10293 Dm NYAALAGNPLLTEYADHSVGAIKQORRLATNREHPYQRATVGVPAKPAGFIEIQ
 QKI-6 Hs --YTLAPATSILEYPIEPSGVLGAVATKVRHDMRVHPYQRIVTADRAATGN--
 QKI-2 Hs --YTLAPATSILEYPIEPSGVLEWIEMPVMP-DISAH-----
 QKI-3 Hs --YTLAPATSILEYPIEPSGVLGMAFPTKG-----
 HQK-7B Hs --YTLAPATSILEYPIEPSGVLGKFFSPWG-----

Figure 12. Expression of human *hox* homologs in mammalian (human) tissue

Figure 12A. Quantitative analysis of Quaking 6 (QKI-6) expression in human abdominal adipocyte cells during the differentiation from preadipocytes to mature adipocytes

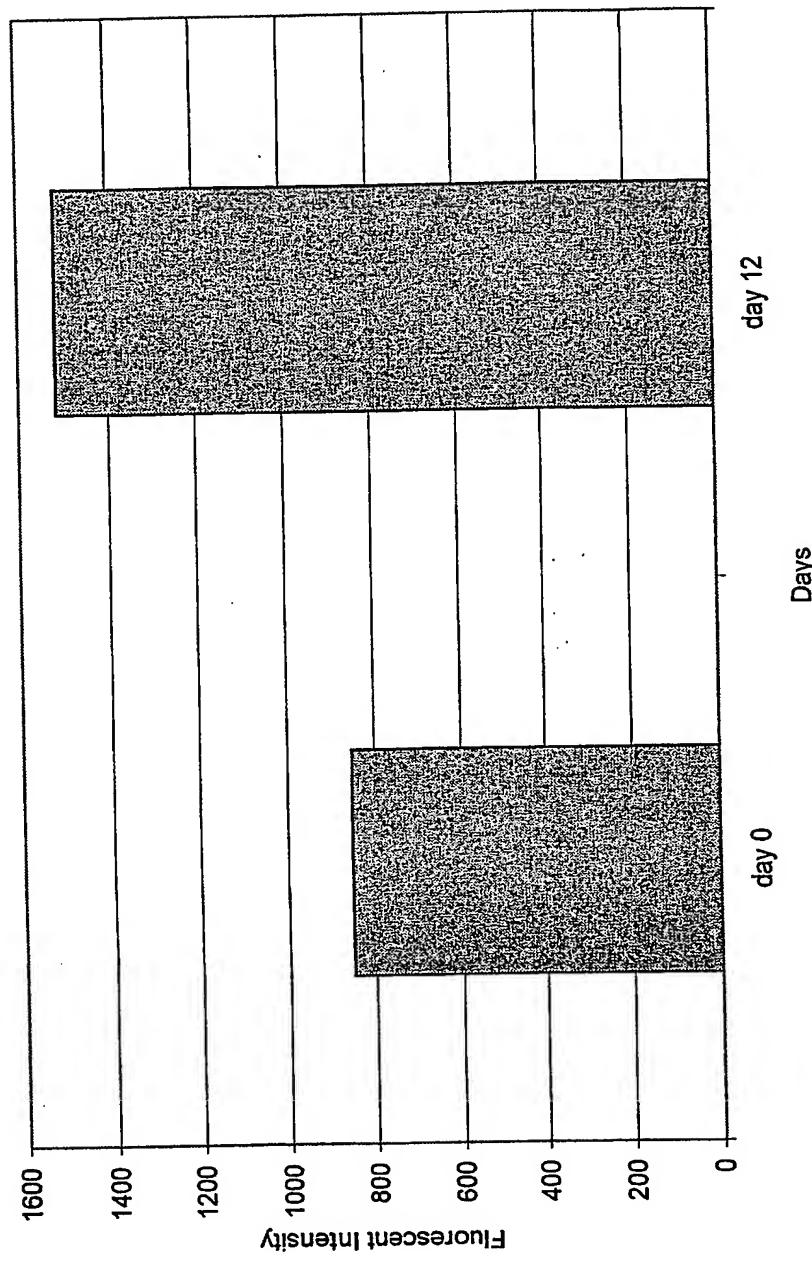


Figure 12B. Quantitative analysis of human RNA binding protein HQK-7B expression in human abdominal adipocyte cells during the differentiation from preadipocytes to mature adipocytes

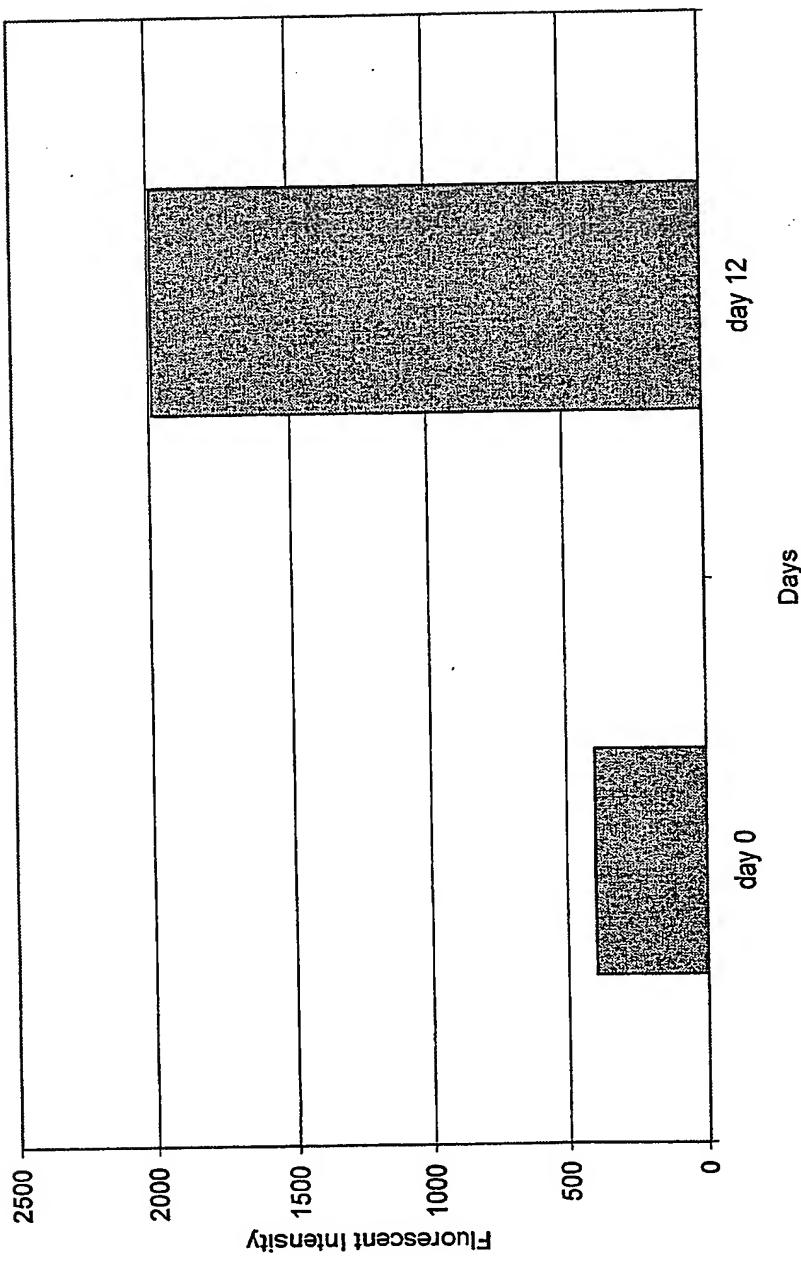
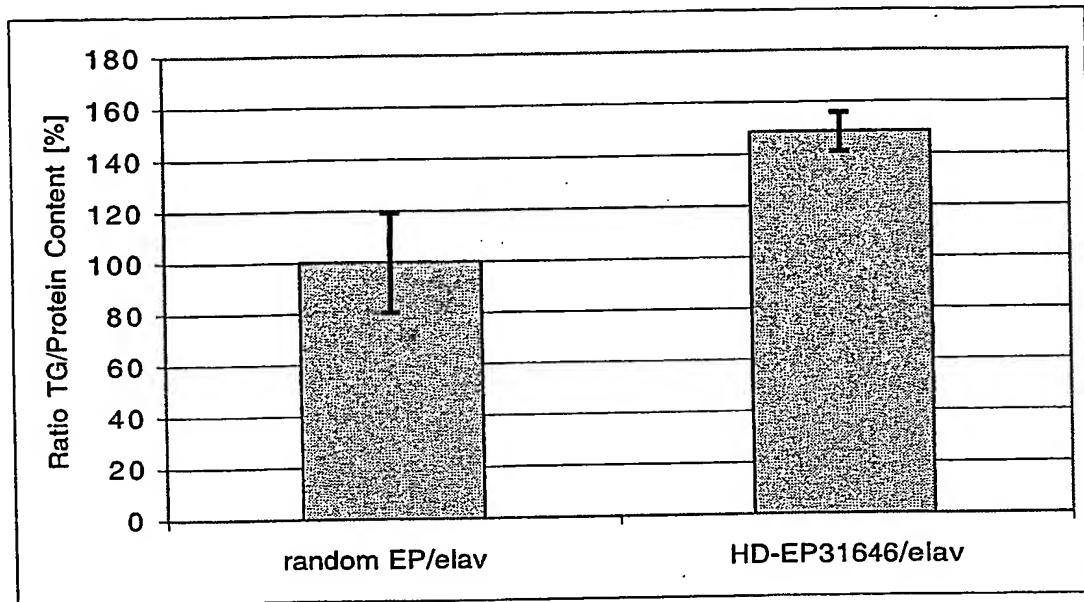


Figure 13. Triglyceride content of a Drosophila CG9373 (GadFly Accession Number) mutant



10/511627

Figure 14. Molecular organisation of the CG9373 gene (GadFly Accession Number)

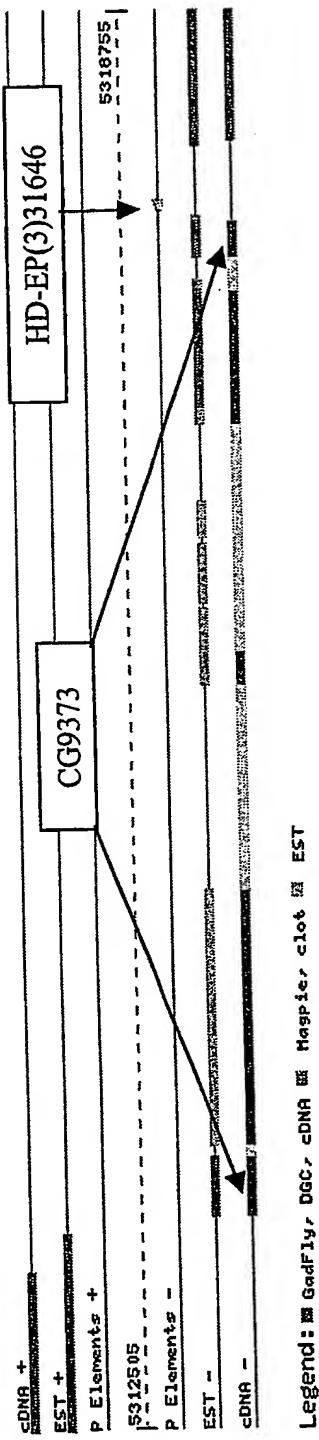


Figure 15. Homology of Drosopila GadFly Accession Number CG9373 to human KIAA1443 protein, human unnamed protein product, and human myelin gene expression factor 2

**Figure 15A. BLASTP results for GadFly Accession Number CG9373
Homology to human protein BAA92579.1 (GenBank Accession Number)**

dbj|BAA92579.1| (AB037762) KIAA1341 protein [Homo sapiens], Length = 620
 Score = 249 bits (635), Expect = 1e-64
 Identities = 207/660 (31%), Positives = 295/660 (44%), Gaps = 148/660 (22%)

Query: 1 MSMDasNSVESREKERDERRGRGAR-GSRFTDADGNGN-GAGSQGGGVAARDRSRERRNCR 58
 + M+ S + + + + G++ +RF + N G G + G RN R
 Sbjct: 72 VKMENDESAKEEKSSDLKEKSTGSKKANRFHPYSKDKNSGTGEKKG-----PNRN-R 121

Query: 59 VVISNIPYDYRWQDLKDLFRRIVGSIEYVQLFFDESGKARGCGIVEFKDPENVQKALEKM 118
 V+ISNIPYD +WQ +KDL R VG + YV+LF D GK+RGCG+VEFKD E V+KALE M
 Sbjct: 122 VFISNIPYDMKWQAIKDLMREKVGEVTYVELFKDAEGKSRGCGVVEFKDEEFVKKALETM 181

Query: 119 NRYEVNGRELVVKEDHGEQRDQYGRIVRDGGGGGGGGVQGGNGGNNGGGGGGRDHMD 178
 N+Y++GR L +KED + + + R GG GG H+
 Sbjct: 182 NKYDLSGRPLNIKEDPDGENARRA-LQRTGGSFPGG-----HVP 219

Query: 179 DRDRGFSRRDDDRSLGRNNFNMMMSNDYNNSSNYNLYGLSASFLESLGISGPLHNKFVAN 238
 D G L NN N+ +N +G L + +FVAN
 Sbjct: 220 DMGSLMLNLPPI---NNPNIPPEVISNLQ-----AGRLGSTIFVAN 259

Query: 239 LDYKVDNKKLKQVFKLAGKVQSVDLSDLKEGNSRGFAVIEYDHPEAVQAISMLDRQMLF 298
 LD+KV KKLK+VF +AG V+ D+ DK+G SRG + ++ +EAVQAISM + Q LF
 Sbjct: 260 LDFKVGWKKLKEVFSIAGTVKRADIKEKDGSRGMTVTFEQIAIEAVQAISMFNGQFLF 319

Query: 299 DRRMTVRLD--RIPDK-----NEGIKLPEGLGGVGIGLGPNGEPLRDVAHNLPNGQSQ 350
 DR M V++D +P + + +LP GLGG+G+GLGP G+P+ N+
 Sbjct: 320 DRPMHVKMDDKSVPHHEEYRSHDGKTPQLPRGLGGIGMGLPGQQPISASQLNI----- 372

Query: 351 GQLLGNAQQSQLGSVGSQPNSAVSNATTNLLNNLTGVMFGNHAQVQPSPVAPVQKPSL 410
 G ++GN G + G FG + +
 Sbjct: 373 GGVMGNLPGGGM-----GMDGPGFGG-----MNRI 397

Query: 411 GNNTGSGGLNLLNNLNPSILA AVVGNLGNQG--GNLSNPLLSSL-----SNLGLNLGNS 462
 G G GGL N +G G G L ++SS+ ++G+N G
 Sbjct: 398 GGGIGFGGLEAMN-----SMGGFGGVGRMGELYRGAMTSSMERDFGRGDIGINRGFG 449

Query: 463 GNDNLPPSNVGLSNYYSSGGTGGGNSYSSGNNSYSGGGSSN-----LGYNAYSSS-G 514
 + L + +G +G G N G+ SGG GS N +G + SSS
 Sbjct: 450 DSFGRIGSAMIG----GFAGRIGSSNMGPVGSGISGGMGSMSNTGGMGMGLDRMSSFD 505

Query: 515 GMGGGNGGVGVGDGNDYNTGNPLDVYGGGSNVGNNSNVGSANAVGASRKSDTIIKNVPITC 574
 MG G G + D + G G G +GS K + I ++N+P
 Sbjct: 506 RMGPGIGAILERSIDMDRGFLSGPMGSGM---RERIGS-----KGNQIFVRNLPFDL 554

Query: 575 TWQTLRDKFREIGDVKFAEI----RGNDVGVRFFKERDAELAIALMDGSRLDGRNIKV 629
 TWOQ L++KF + G V FAEI + G VRF AE A +M+G ++ GR I V
 Sbjct: 555 TWQKLKEKF SQCGHVMFAEIKMENGKSKCGTVRFDSPESAEKACRIMNGIKISGREIDV 614

Score = 68.6 bits (166), Expect = 2e-10
 Identities = 41/114 (35%), Positives = 67/114 (57%), Gaps = 6/114 (5%)

Query: 20 GRGARGSRFTDADGNNGAGSQGGGVAARDRSRERRNCRVYISNI PYDYLWQDLKDLFRR 79
 G GA R D D G +G G G+ R+R + N +++++ N+P+D WQ LK+ F +
 Sbjct: 510 GIGAILERSIDMD-RGFLSGPMGSGM--RERIGSKGN-QIFVRNLPFDLTWQKLKEKFQS 565

Query: 80 IVGSIEYVQLFFDESGKARGCGIVEFKDPENVQKALEKMRYEVNGRELVVKED 133
 G + + ++ E+GK++GCG V F PE+ +KA MN +++GRE+ V+ D
 Sbjct: 566 C-GHVMFAEIKM-ENGKSKCGTWRFDSPESAEKACRIMNGIKISGREIDVRLD 617

Score = 56.2 bits (134), Expect = 1e-06
 Identities = 46/180 (25%), Positives = 76/180 (41%), Gaps = 21/180 (11%)

Query: 139 DQYGRIVRDGGGGGGG-----GGVGQGGNGGNNGGGGGGRDHMDDRDRGFSSRD 188
 D +GR+ GG G G G+ GG G N GG G +D F R
 Sbjct: 450 DSFGRLGSAMIGGFAGRIGSSNMGPVGSGISGGMGSMNSVTGGMGMG-LDRMSSSFDRM- 507

Query: 189 DDRLSGRNNFNMMMSNDYNNSSNYNLYGLSASFLES LGISGPLHNKV FVANLDYKVDNKKL 248
 G ++ + + + + E +G G N+FV NL + + +KL
 Sbjct: 508 -----GPGIGAILERSIDMDRGFLSGPMGSGMRERIGSKG---NQIFVRNLPFDLTWQKL 559

Query: 249 KQVFKLAGKVQSVDSLSDKEGNSRGFAVIEYDH PVEAVQAISMLDRQMLFDRRMTVRLDR 308
 K+ F G V ++ + + G S+G + +D P A +A +++ + R + VRLDR
 Sbjct: 560 KEKFSQC GHVMFAEIKMEN-GKS KGCGTWRFDSPESAEKACRIMNGIKISGREIDVRLDR 618

Homology to human protein BAB14421.1 (GenBank Accession Number)

>dbj|BAB14421.1| (AK023133) unnamed protein product [Homo sapiens],
 Length = 576

Score = 242 bits (618), Expect = 1e-62
 Identities = 206/654 (31%), Positives = 289/654 (43%), Gaps = 160/654 (24%)

Query: 1 MSMDASNSVESREKERDERRGRGAR-GSRFTDADGNGN-GAGSQGGGVAARDRSRERRNCR 58
 + M+ S + + + + G++ +RF + N G G + G RN R
 Sbjct: 52 VKMENDESAKEEKS DKEKSTGSKKANRFHPYSKDKNSGTGEKKG-----PNRN-R 101

Query: 59 VYISNIPYD YRQDLKDLFRRIVGSIEYVQLFFDESGKARGCGIVEFKDPENVQKALEKM 118
 V+ISNIPYD +WQ +KDL R VG + YV+LF D GK+RGCG+VEFKD E V+KALE M
 Sbjct: 102 VFISNIPYDMKWQAIK DLMREKVGEVTVYELFKDAEGKSRGCGV EFKDEEFVKKALET M 161

Query: 119 NRYEVNGRELVVKED-HGEQRDQYGRIVRDGGGGGGGGVQGGNGGNNGGGGGGRDHM 177
 N+Y+++GR L +KED GE + + R GG GG H+
 Sbjct: 162 NKYDLSGRPLNIKEDPDGENARRASQ--RTGGSFPGG-----HV 198

Query: 178 DDRDRGFSRRDDRLSGRNNFNMMMSNDYNNSSNYNLYGLSASFLES LGISGPLHNKV FVA 237
 D G L NN N+ +N +G L + +FVA
 Sbjct: 199 PDMGSGLMNLPPSIL---NNPNIPPEVISNLQ-----AGRLGSTIFVA 238

Query: 238 NLDYKVDNKKLQVF KLAGKVQSVDSLSDKEGNSRGFAVIEYDH PVEAVQAISMLDRQML 297
 NLD+KV KKLK+VF +AG V+ D+ DK+G SRG + ++ +EAVQAISM + Q L
 Sbjct: 239 NLDFKVGVKKLKEVFSIAGTVKRADIKEDKDGSRGMTVTFEQAIIEAVQAISM FNGQFL 298

Query: 298 FDRRMTVRLD--RIPDK-----NEGIKLPEGLGGVGIGLGPNGEPLRDVAHNLPNGQOS 349

FDR M V++D +P + +LP GLGG+G+GLGP G+P+ N+
 Sbjct: 299 FDRPMHVKMDDKSVPHEEYRSHDGKTPQLPRGLGGIGMGLPGQQPISASQLNI----- 352

Query: 350 QGQLLGNAQQGSQQLGSVGSQPNSAVSNATTNLLNNLTGVMFNHAAVQPSPVAPVQKPS 409
 G ++GN G + G FG
 Sbjct: 353 -GGVMGNLGPGGM-----GMDGPFGGG-----MNR 376

Query: 410 LGNNNTGSGGLNLNNLNPSILAAVGNLGNQG--GNLSNPPLSSSL-----SNLGLNLGN 461
 +G G GGL N +G G G L ++SS+ ++G+N G
 Sbjct: 377 IGGGIGFGGLEAMN-----SMGGFGGVGRMGELYRGAMTSSMERDFGRGDIGINRG- 427

Query: 462 SGNDNLPPSNVGLSNYYSSGGTGGGSNSYSSGNNYSGGGSSNLGYNAYSSS-GGMGGGN 520
 G S GG GG NS + G +G + SSS MG G
 Sbjct: 428 -----FGDSFGRLLGGGMGGMNSVT-----GGMGMGLDRMSSSFDRMGPPI 467

Query: 521 GGVGVGDNDYNTGNPLDVYGGGSNVGSANAVGASRKSDTIIIKNVPICTWQTLR 580
 G + D + G G G +GS K + I ++N+P TWQ L+
 Sbjct: 468 GAILERSIDMDRGFLSGPMGSGM---RERIGS-----KGNQIFVRNLPFDLTWQKLK 516

Query: 581 DKFREIGDVKFAEI-----RGNDVGVRFFKERDAELAIALMDGSRLDGRNIKV 629
 +KF + G V FAEI + G VRF AE A +M+G ++ GR I V
 Sbjct: 517 EKFSQCGHVMFAEIKMENGKSKCGTWRFDSPESAEKACRIMNGIKISGREIDV 570

Score = 72.8 bits (177), Expect = 1e-11
 Identities = 82/348 (23%), Positives = 133/348 (37%), Gaps = 96/348 (27%)

Query: 54 RRNCRVYISNIPYDYLWQDLKDLFRRIVGSIEYVQLFFDESGKARGCGIVEFKDPENVQK 113
 R +--+ + W+ LK++F I G++ + D+ GK+RG G V F+ +
 Sbjct: 230 RLGSTIFVANLDFKVGWKKLKEVFS-IAGTVKRADIKEDKDGSRGMTVTFEQAIIEAVQ 288

Query: 114 ALEKMNRYEVNGRELVVKED-----HGEQRDQYGRIVRDGGGGGGGG----- 155
 A+ N + R + VK D H E R G+ + G GG G
 Sbjct: 289 AISMFNGQFLFDRPMHVKMDDKSVPHEEYRSHDGKTPQLPRGLGGIGMGLPGQQPISAS 348

Query: 156 -----GGVQG-----GNGGNNGGGG-----GGRDHMDDRDRGF 184
 GGV G G GG N GGG GG M + RG
 Sbjct: 349 QLNIGGVMGNLGPGGMMDGPGFGGMRIGGGIGFGGLEAMNSMGGFGGVGRMGELYRGA 408

Query: 185 SRRDDDRLSGRNNFNMMS-----NDYNNSSNYNLYGLSASFLESLG--- 225
 +R GR + + N L +S+SF + +G
 Sbjct: 409 MTSSMERDFGRGDIGINRGFGDSFGRLLGGMGGMNSVTGGMGMGLDRMSSSF-DRMGPPI 467

Query: 226 -----ISGPLH-----NKVFVANLDYKVDNKKLKQVFKLAGKVQS 260
 +SGP+ N++FV NL + + +KLK+ F G V
 Sbjct: 468 GAILERSIDMDRGFLSGPMGSGMRERIGSKGNQIFVRNLPFDLTWQKLKEKFSQCGHVMF 527

Query: 261 VDLSLDKEGNSRGFAVIEYDHPVEAVQAISMLDRQMLFDRRMTVRLDR 308
 ++ ++ G S+G + +D P A +A +++ + R + VRLDR
 Sbjct: 528 AEIKMEN-GKSKGCGTWRFDSPESAEKACRIMNGIKISGREIDVRLDR 574

Score = 68.6 bits (166), Expect = 2e-10
 Identities = 41/114 (35%), Positives = 67/114 (57%), Gaps = 6/114 (5%)

Query: 20 GRGARGSRFTDADGNNGNGAGSQGGGVAARDRSRERRNCRVYISNIPYDYLWQDLKDLFRR 79
 G GA R D D G +G G G+ R+R + N +--+ N+P+D WQ LK+ F +
 Sbjct: 466 GIGAILERSIDMD-RGFLSGPMGSGM--RERIGSKGN-QIFVRNLPFDLTWQKLKEKFSQ 521

Query: 80 IVGSIEYVQLFFDESGKARGCGIVEFKDPENVQKALEKMNRYEVNGRELVVKED 133

10/511627

WO 03/092715

PCT/EP03/04650

32/51

G + + ++ E+GK++GCG V F PE+ +KA MN +++GRE+ V+ D
Sbjct: 522 C-GHVMFAEIKM-ENGKSKCGTVRFDSPESAEKACRIMNGIKISGREIDVRLD 573

Homology to human protein NP057216.1 (GenBank Accession Number)

ref|NP_057216.1| (NM_016132) myelin gene expression factor 2 [Homo sapiens]
gb|AAD43038.1| (AF106685) myelin gene expression factor 2 [Homo sapiens]
Length = 547

Score = 238 bits (607), Expect = 2e-61
Identities = 204/659 (30%), Positives = 295/659 (43%), Gaps = 150/659 (22%)

Query: 3 MDASNSVESREKERDRRGAR-GSRFTDADGNGN-GAGSQGGGVAARDRSRERRNCRVY 60
M+ S + + + + G++ +RF + N G G + G . RN RV+
Sbjct: 1 MENDESAKEEKSSDLKEKSTGSKKANRFHPYSKDKNSGTGEKKKG-----PNRN-RVF 50

Query: 61 ISNIPYDYRWQDLKDLFRRIVGSIEYVQLFFDESGKARGCGIVEFKDPENVQKALEKMNR 120
ISNIPYD +WQ +KDL R VG + YV+LF D GK+RGC+VEFKD E V+KALE MN+
Sbjct: 51 ISNIPYDMKWQAIKDLMREKVGEVTYVELFKDAEGKSRGCGVVEFKDEFVKKAETMNK 110

Query: 121 YEVNGRELVVVEDHGEQRDQYGRIVRDGGGGGGGGVQGGNGGNNGGGGGGRDHMDDR 180
Y+++GR + +KED + + + R G QG + + G G
Sbjct: 111 YDLSGRRVNNIKEDPDGENARRA-LQRTGTS-----FQGSHASDVGSG----- 151

Query: 181 DRGFSRRDDDRSLGRNNFNMMSSNDYNNSNNLYGLSASFLES LGISGPLHNVFVANLD 240
N+ + NN + + + +L +G L + +FVANLD
Sbjct: 152 -----LVNLPPSILNNP-----IPPEVISNLQ-AGRLGSTIFVANLD 188

Query: 241 YKVDNKKLKQVFKLAGKVQSVDSLDEGNSRGFAVIEYDH PVEAVQAISMLDRQMLFDR 300
+KV KKLK+VF +AG V++ DK+G SRG + ++ +EAVQAISM + Q LFDR
Sbjct: 189 FKVGWKKLKEVFSTIAGTVKAGSYKEDKDGSRGMTVTFEQAIIEAVQAISMNGQFLFDR 248

Query: 301 RMTVRLD-----RIPDKNEGIKLPEGLGGVGIGLGPNGEPLRDVAHNLPNGGQSQG 351
M V++D R PD + +LP GLGG+G+GLGP G+P+ N+ G
Sbjct: 249 PMHVVKMDDKSVPHEEYRSPD-GKTPQLPRGLGGIGMGLGPQQPISASQLN-----G 300

Query: 352 QLLGNAQQSQLGSVGSQPNSAVSNATTNLLNLTGVMFGNHAAVQPSPVAPVQKPSLG 411
++GN G + G FG + G
Sbjct: 301 GVMGNLGPCCG-----GMDGPGFGG-----MNRIG 325

Query: 412 NNTGSGGLNLNNLNPSILA AVVGNLGNQG--GNLSNPLLSSLS-----NLGLNLGNSG 463
G GGL N +G G G G L ++SS+ ++GL+ G
Sbjct: 326 GGI GF GG LEAMN-----SMGGFGGVGRMGELYRGAMTSSMERDFGHRDIGLSRGFGD 377

Query: 464 NDDNLPPSNVGLSN NYSSGGTGGGNSYSSGNNYSGGGSSN-----LGYNAYSSS-GG 515
+ L + +G +G G N G+ SGG GS N +G + SSS
Sbjct: 378 SFGRIGSSNMGPVGSGISGGMGSMSVTGGMGMGLDRMSSSFDR 433

Query: 516 MGGGNGGVGVGDNDYNTGNPLDVYGGGSNVGSANAVGASRKSDTIIIKNVPITCT 575
MG G G + D + G G G +GS K + I ++N+P T
Sbjct: 434 MGPGIGAILERSIDMDRGFLSGPMGSGM---RERIGS-----KGNQIFVRNLPFDLT 482

Query: 576 WQTLRDKFREIGDVKFAEI-----RGNDVGVVRFFKERDAELAIALMDGSRLDGRNIKV 629
WQ L++KF + G V FAEI + G VRF AE A +M+G ++ GR I V
Sbjct: 483 WQKLKEFKSQCQGHVMFAEIKMENGKSKCGTVRFDSPESAEKACRIMNGIKISGREIDV 541

Score = 68.6 bits (166), Expect = 2e-10
 Identities = 41/114 (35%), Positives = 67/114 (57%), Gaps = 6/114 (5%)

Query: 20 GRGARGSRFTDADGNNGNAGSQGGGVAAARDRSRERRNCRVYISNIPYDQRWQDLKDLFRR 79
 G GA R D D G +G G G+ R+R + N +++++ N+P+D WQ LK+ F +
 Sbjct: 437 GIGAILERSIDMD-RGFLSGPMGSGM--RERIGSKGN-QIFVRNLPFDLTWQKLKEKFSQ 492

Query: 80 IVGSIEYVQLFFDESGKARGCGIVEFKDPENVQKALEKMNRYEVNGRELVVKED 133
 G + + ++ E+GK++GCG V F PE+ +KA MN +++GRE+ V+ D
 Sbjct: 493 C-GHVMFAEIKM-ENGKSKCGTVRFDSPESAEKACRIMNGIKISGREIDVRLD 544

Score = 55.5 bits (132), Expect = 2e-06
 Identities = 41/157 (26%), Positives = 69/157 (43%), Gaps = 11/157 (7%)

Query: 152 GGGGGGVQGGNGGNNGGGGGGRDHMDDRRGFSRRDDDRLSGRNNFNMMNSNDYNNSSNY 211
 G G G+ GG G N GG G +D F R G ++ + + +
 Sbjct: 400 GPVGSGISGGMGSMSVTGGMGMG-LDRMSSSFDRM-----GPGIGAILERSIDMDRGF 452

Query: 212 NLYGLSASFLES LGI SGPL HNKVF VAN LDYKV DNKKL QVF KLAG KVQS VL SLDKE GNS 271
 + + E +G G N++F V NL + + +KLK+ F G V ++ ++ G S
 Sbjct: 453 LSGPMGSGMRERIGSKG--NQIFVRNLPFDLTWQKLKEKFSQCGHVMFAEIKMEN-GKS 508

Query: 272 RGFAVIEYDHPVEAVQAISMLDRQMLFDRRMTVRLDR 308
 +G + +D P A +A + + + R + VRLDR
 Sbjct: 509 KGCGTVRFDSPESAEKACRIMNGIKISGREIDVRLDR 545

Figure 15B. Multiple Sequence Alignment (ClustalW 1.83)

CG9373	Dm	-----	
KIAA1341	Hs	PLSRSEPLSSGGRGGGSGGGMADANKAEVPGATGGDSPHLQPAEPGEPREPHPAEEAK	
MyEF-2	Hs	-----	
FLJ13071	Hs	-----MADANKAEVPGATGGDSPHLQPAEPGEPREPHPAEEAK	
CG9373	Dm	---MSMDASNSVESREKERDRRGRGARGSRFTDADGNNGAGSQGGVAARDRSRERRNC	
KIAA1341	Hs	QQPQHSSSSNGVKMENDESAKEEKSDLKEKSTGSKKANRFHPYSKDKNSGTGEKKGPNRN	
MyEF-2	Hs	-----MENDESAKEEKSDLKEKSTGSKKANRFHPYSKDKNSGTGEKKGPNRN	
FLJ13071	Hs	QQPQHSSSSNGVKMENDESAKEEKSDLKEKSTGSKKANRFHPYSKDKNSGTGEKKGPNRN	
CG9373	Dm	RVYISNIPYDYRWQDLKDLFRRIVGSIEYYQLFFDESGKARGCGIVEFKDPENVQALEK	
KIAA1341	Hs	RVFISNIPYDMKWQAIKDLMREKVGEVTYVELFKDAEGKSRGCGVVEFKDEEFVKKALET	
MyEF-2	Hs	RVFISNIPYDMKWQAIKDLMREKVGEVTYVELFKDAEGKSRGCGVVEFKDEEFVKKALET	
FLJ13071	Hs	RVFISNIPYDMKWQAIKDLMREKVGEVTYVELFKDAEGKSRGCGVVEFKDEEFVKKALET	
CG9373	Dm	MNRYEVNGRELVVKEDHGEQRDQYGRIVRDGGGGGGGGVQGGNGGNNGGGGGGRDHM	
KIAA1341	Hs	MNKYDLSGRPLNIKEPDGENARR-----ALQRTGGSFPGGHVPDMSG-----	
MyEF-2	Hs	MNKYDLSGRRVNIKEPDGENARR-----ALQRTGTSFQGSHASDVGSG-----	
FLJ13071	Hs	MNKYDLSGRPLNIKEPDGENARR-----ASQRTGGSFPGGHVPDMSG-----	
CG9373	Dm	DDRDRGFSRRDDRLSGRNNFNMMSDNDYNNSSNYNLGLSASFLESLGIISGPLHNKFVA	
KIAA1341	Hs	-----LMNLPPSILNNPNPIPPEVISNLQ-----AGR LGSTIFVA	
MyEF-2	Hs	-----LVNLPPSILNNPNPIPPEVISNLQ-----AGR LGSTIFVA	
FLJ13071	Hs	-----LMNLPPSILNNPNPIPPEVISNLQ-----AGR LGSTIFVA	

CG9373 Dm NLDYKVDNKKLKQVFKLAGKVQSVDSLSDKEGNSRGFAVIEYDHVEAVQAISMLDRQML
 KIAA1341 Hs NLDFKVGWKKLKEVFSIAGTVKRADIKEDKDGSRGMTVTFEQAIEAVQAISMFNGQFL
 MyEF-2 Hs NLDFKVGWKKLKEVFSIAGTVKAGSYKEDKDGSRGMTVTFEQAIEAVQAISMFNGQFL
 FLJ13071 Hs NLDFKVGWKKLKEVFSIAGTVKRADIKEDKDGSRGMTVTFEQAIEAVQAISMFNGQFL

CG9373 Dm FDRRMTVRLLDRIPDKNEGIK-----LPEGLGGVGIGLGPNGEPLRDVAHNLPNGGQS
 KIAA1341 Hs FDRPMHVKMDDKSVPHHEEYRSHDGKTPQLPRGLGGIGMGLGPGGQPISASQLNIG-----
 MyEF-2 Hs FDRPMHVKMDDKSVPHHEEYRSPDGKTPQLPRGLGGIGMGLGPGGQPISASQLNIG-----
 FLJ13071 Hs FDRPMHVKMDDKSVPHHEEYRSHDGKTPQLPRGLGGIGMGLGPGGQPISASQLNIG-----

CG9373 Dm QGQLLGNAQQGSQLGSVGSQPNSSAVSNATTNLLNNLTG-VMFGNHAAVQPSPVAPVQKP
 KIAA1341 Hs -----GVMGNLG--PGGMGMDGPGFGGMNRIGGGIGFGGLEAMN-----
 MyEF-2 Hs -----GVMGNLG--PGGMGMDGPGFGGMNRIGGGIGFGGLEAMN-----
 FLJ13071 Hs -----GVMGNLG--PGGMGMDGPGFGGMNRIGGGIGFGGLEAMN-----

CG9373 Dm SLGNNTGSGGLNLLNNLNPSILA VVGNLGNQGGNLSNPLSSSLNGLNLGNSGNDDNL
 KIAA1341 Hs SMGGFGGVG--RMGELYRGAMTSSMERDFGRGDIGINRGFGDSFGRGSA -IGGFAGRI
 MyEF-2 Hs SMGGFGGVG--RMGELYRGAMTSSMERDFGRHDIGLSRGFGDSFGRGSA -IGGITGRI
 FLJ13071 Hs SMGGFGGVG--RMGELYRGAMTSSMERDFGRGDIGINRGFGDSFGRG-----

CG9373 Dm PPSNVGLSNNYSSGGTGGGNSYSSGNNSYSGGGSSNLGYNAYSSSGGMGGGGNGGVVDGN
 KIAA1341 Hs GSSNMGPVVGSGISGGMGSMNSVTGGMGMGLDRMSSSFDR-----MGPGIGAILERSI
 MyEF-2 Hs GSSNMGPVVGSGISGGMGSMNSVTGGMGMGLDRMSSSFDR-----MGPGIGAILERSI
 FLJ13071 Hs -----GGMGMNSVTGGMGMGLDRMSSSFDR-----MGPGIGAILERSI

CG9373 Dm DYNTGNPLDVYGGGSNVGSNSVGSANAVGASRKSDTIIIKNVPICTCTWQTLRDKFREIGD
 KIAA1341 Hs DMDRG-----FLSGPMGSGMRERIGSKGNQIFVRNLPFDLTWQKLKEKFQSQCGH
 MyEF-2 Hs DMDRG-----FLSGPMGSGMRERIGSKGNQIFVRNLPFDLTWQKLKEKFQSQCGH
 FLJ13071 Hs DMDRG-----FLSGPMGSGMRERIGSKGNQIFVRNLPFDLTWQKLKEKFQSQCGH

CG9373 Dm VKFAEIRGN-----VGVRFFKERDAELAIALMDGSRLDGRNIKVTF---
 KIAA1341 Hs VMFAEIKMENGKSKCGTVERFDSPESAEKACRIMNGIKISGREIDVRLDRNA
 MyEF-2 Hs VMFAEIKMENGKSKCGTVERFDSPESAEKACRIMNGIKISGREIDVRLDRNA
 FLJ13071 Hs VMFAEIKMENGKSKCGTVERFDSPESAEKACRIMNGIKISGREIDVRLDRNA

Figure 16. Expression of CG9373 Homologs in Mammalian Tissues

Figure 16A. Real-time PCR analysis of myelin gene expression factor 2 (MEF-2) expression in wild type mouse tissues
($\Delta\Delta Ct$ Pancreas = 20.90)

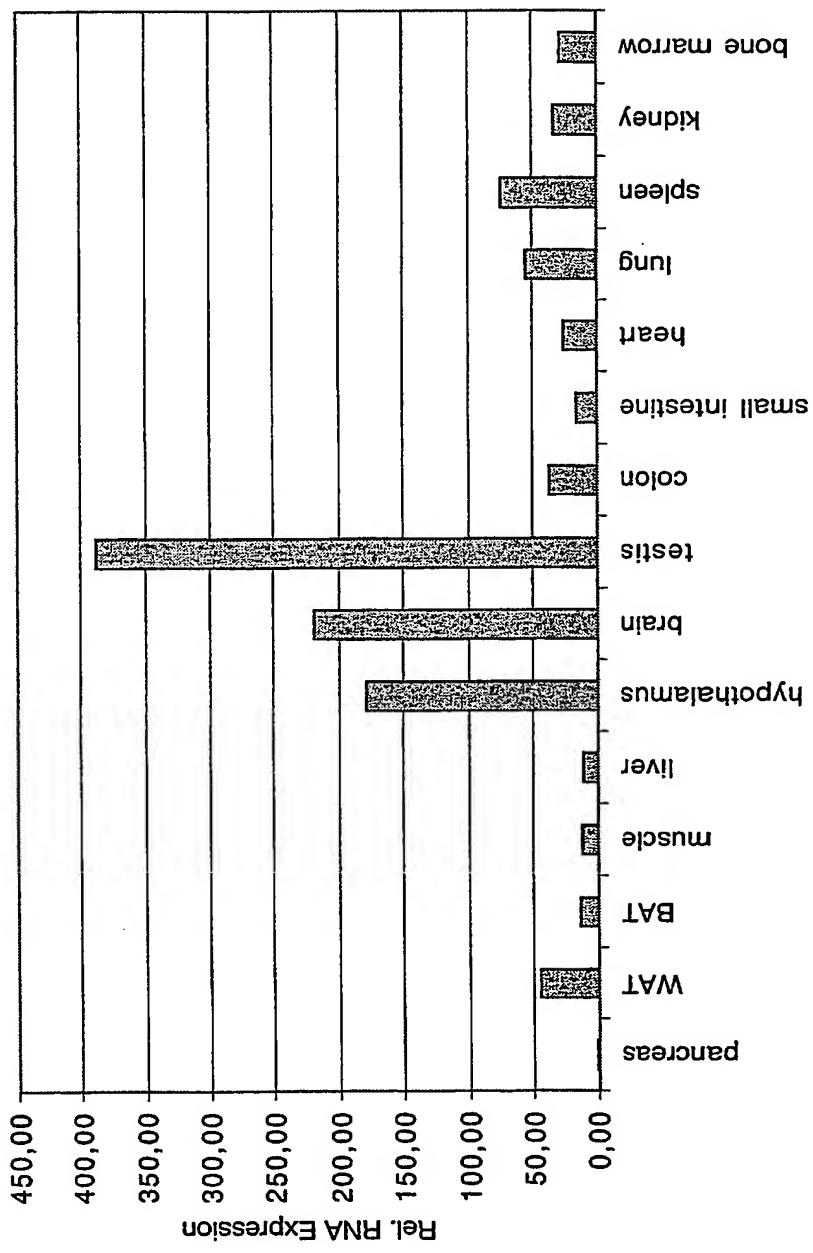


Figure 16B. Real-time PCR analysis of myelin gene expression factor 2 (MEF-2) expression in different mouse models

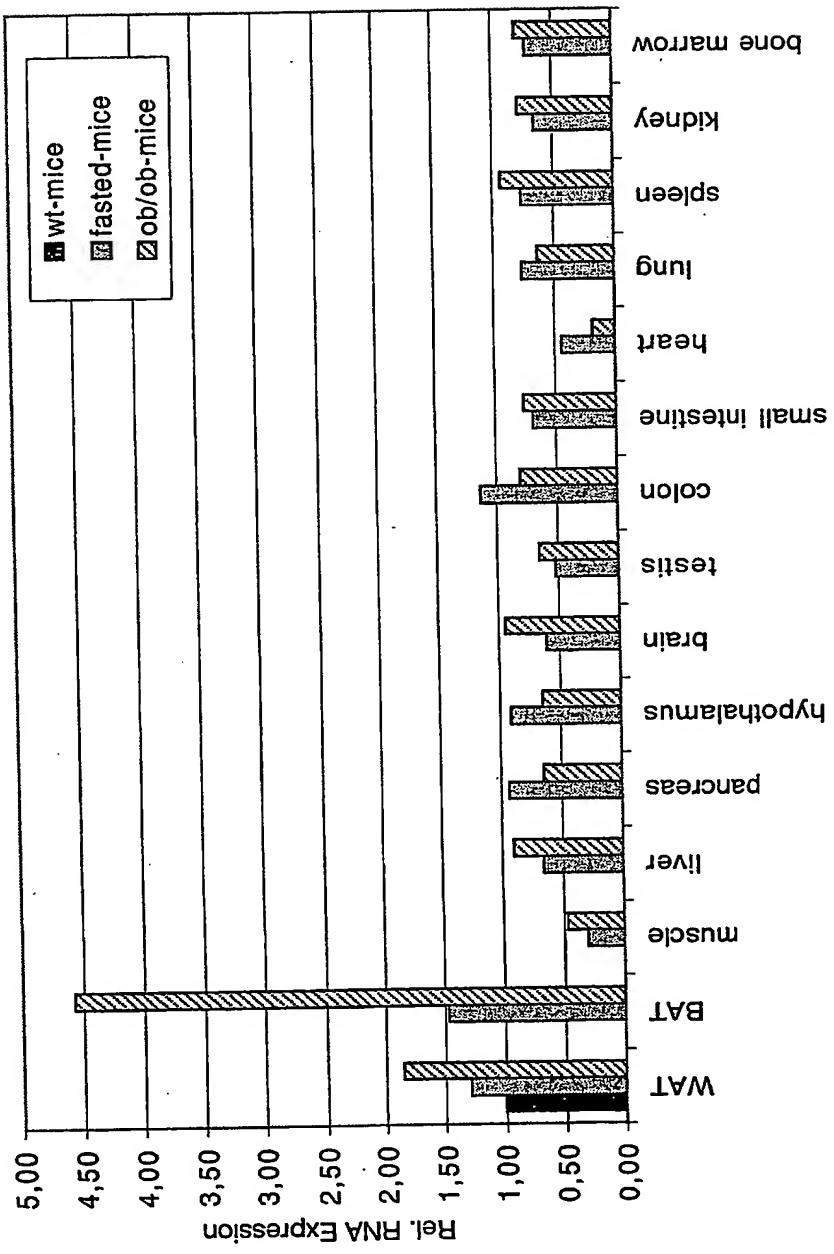


Figure 16C. Real-time PCR analysis of myelin gene expression factor 2 (MEF-2) expression in mice fed with a high fat diet compared to mice fed with a standard diet

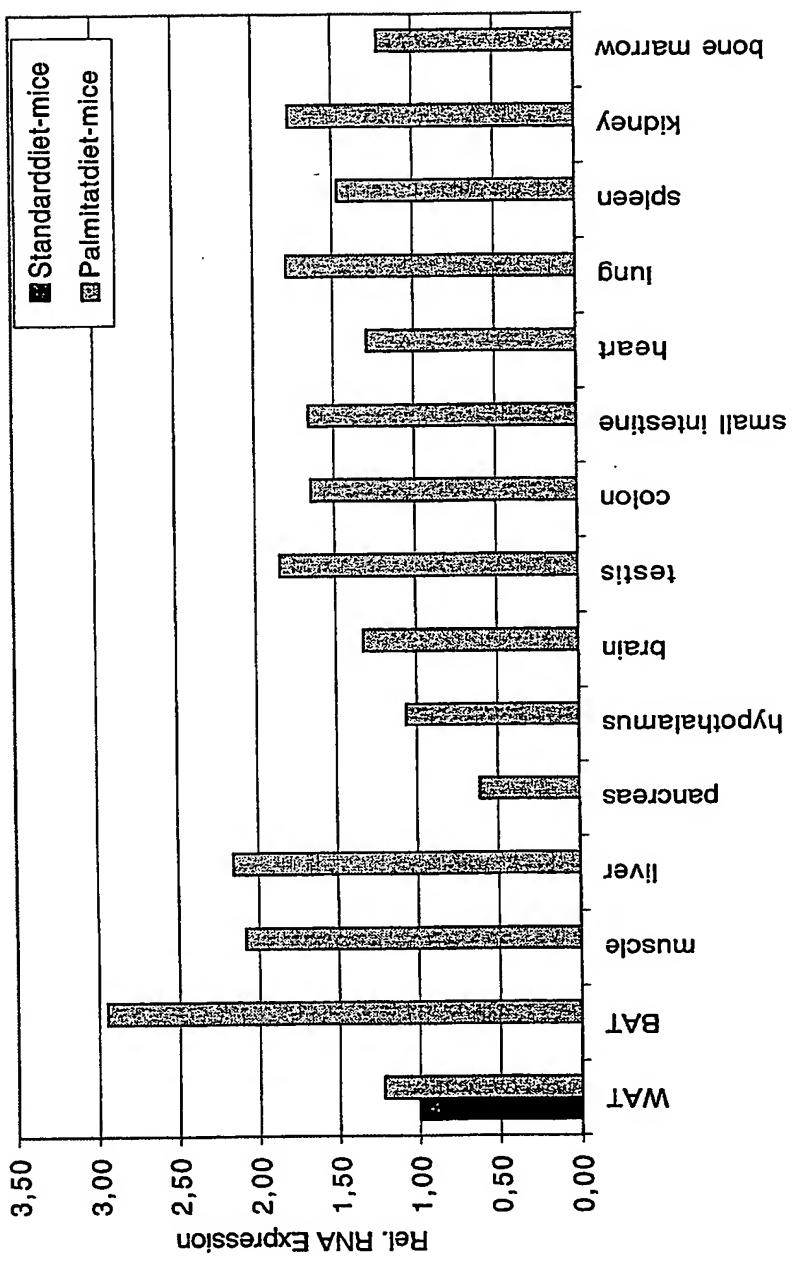


Figure 17. Triglyceride content of a *Drosophila cpo* (GadFly Accession Number CG18434) mutant

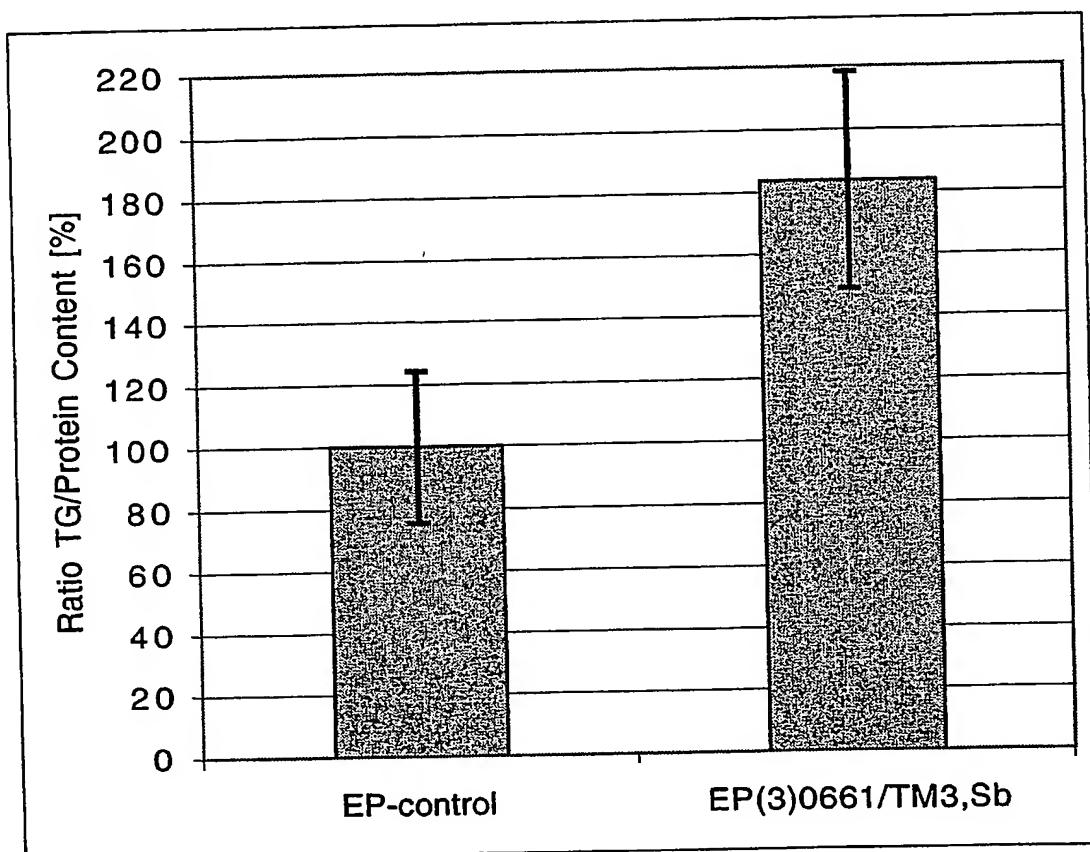


Figure 18. Molecular organisation of the *cpo* gene (GadFly Accession Number CG18434)

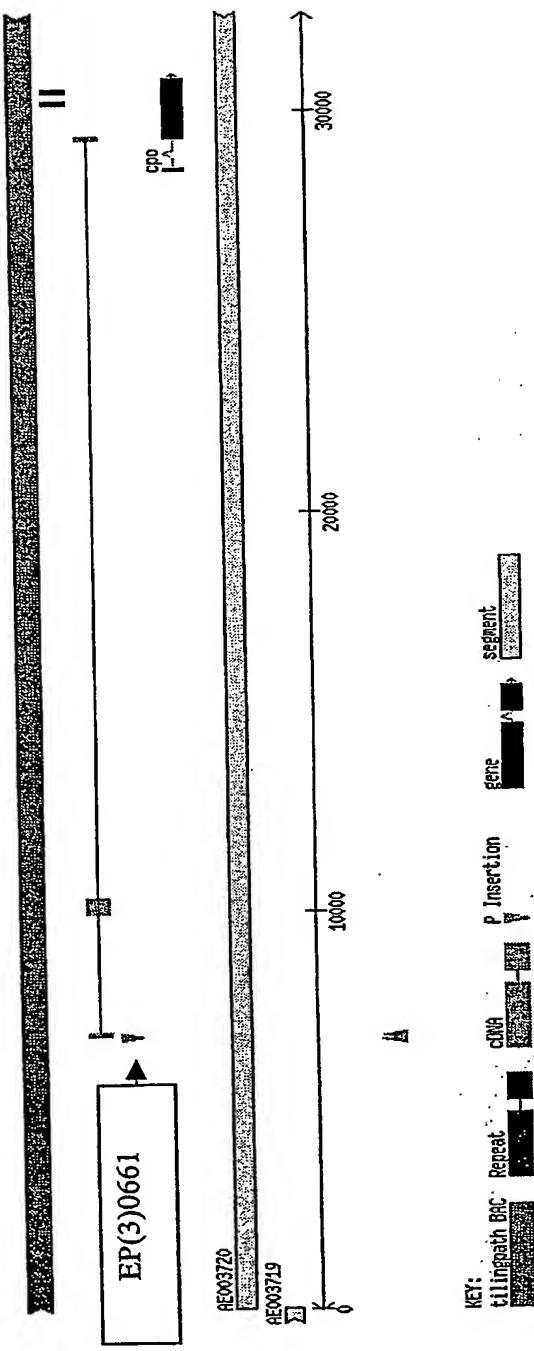


Figure 19. Homology of *Drosopila cpo* (GadFly Accession Number CG31243 and CG18434) to human RNA binding proteins with multiple splicing

Figure 19A. Multiple Sequence Alignment (ClustalW 1.83)

cpo Dm	LVKIANYQDLLGSHHQLLIAATAAAAAAAEPQLQLQHLLPAAPTPAVISNPINSIGP
NP_006858 Hs	-----
IPI00161102 Hs	-----
cpo Dm	INQISSLSSHPNNNQQAVFEKAITISSIAIKRRPTLPQTPASAPQVLSPPSPKRQCAAavs
NP_006858 Hs	-----
IPI00161102 Hs	-----
cpo Dm	VLPVTVPVPVPVSPLPVSVPPVSVKGHPISHTHQIAHTHQISHSHPISHPHHHQLSFA
NP_006858 Hs	-----
IPI00161102 Hs	-----
cpo Dm	HPTQFAAAVAAHQQQQQQQQQQQQQQAVQQQQQQAVQQQQVAYAVAASPQLQQQQQQQH
NP_006858 Hs	-----
IPI00161102 Hs	-----
cpo Dm	RLAQFNQAAAALLNQHLQQQHQAAQQQQHQAAQQQLAHYGGYQLHRYAPQQQQQHILLSS
NP_006858 Hs	-----
IPI00161102 Hs	-----
cpo Dm	GSSSSKHNSNNNSNTSAGAASAAVPIATSVAAVPTTGGSLPDSPAHEHSHESENATASA
NP_006858 Hs	-----
IPI00161102 Hs	-----
cpo Dm	PTTPSPAGSVTSAAPTATATAAAGSAAATAATGTATSAVSDSNNLNSSSNSNSN
NP_006858 Hs	-----
IPI00161102 Hs	-----
cpo Dm	AIMENQMALAPLGLSQSMDSVNTASNEEVRTLTVSGLPMDAKPRELYLLFRAYEGYEGR
NP_006858 Hs	AEKENTPSEANL-----QEEEVRTLTVSGPLDIKPRELYLLFRPFKGYEGS
IPI00161102 Hs	-----QVRTLFVSGLPVDIKPRELYLLFRPFK-----
cpo Dm	LLKVTSKNGKTASPGFVTFHTRAGAEAAKQDLQGVRFDPDMPQTIRLEFAKSNTKVSKP
NP_006858 Hs	LIKLTSKQ----PGFVSDSRSEAAKNALNGIRFDPEIPQTLREFAKANTKMAKN
IPI00161102 Hs	-----PGFVTFDSRAGAEAAKNALNGIRFDPENPQTLREFAKANTKMAKS
cpo Dm	KPQPNTATTASHPALMHPLTG-----HLGGPFFPGGPELWHHPLAYSAAAAAELPG---
NP_006858 Hs	KLVGTPNPSTPLPNTVPQFIAREPYELTVPALYPSSPEVWAPYPLYPAELAPALPPAFT
IPI00161102 Hs	KLMATPNPSNVHPALGAHFIARDPYDLMGAALIPASPEAWAPYPLYTELTPAISHAAFT
cpo Dm	-----AAALQHATLVHPALHPQVP---VRSYL
NP_006858 Hs	YP-----ASLHAQMWRWLPPSEATSQGWKSQFC
IPI00161102 Hs	YPTATAAAALHAQVRWYPSSDTTQQGWKYRQFC

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FIGURE 19B. Amino acid sequence encoded by Drosophila gene CG31243 (GadFly Accession Number), SEQ ID NO:1

>CG31243-PA (AE003720) [gene_syn=CG31243] [prot_desc=CG31243 gene product from transcript CG31243-RA]

1 LVKIANYODL LGSHHQLLIA ATAAAAAAA AEPQLQLQHL LPAAPTTPAV ISNPINSIGP
61 INQISSLSSHP SNNNQQAVFE KAITISSIAI KRRPTLPQTP ASAPQVLSPS PKRQCAA AVS
121 VLPVTVPVPV PVSPLPVSV PVPVSVKGHP ISHTHQIAHT HQISHSHPIS HPHIHQLSFA
181 HPTQFAAAVA AHHQQQQQQQ AQQQQQAVQQ QQQQAVQQQQ VAYAVAASPO LQQQQQQQQH
241 RLAQFNQAAA AALLNQHLQQ OHQAQQQQHQ AQQOSLAHYG GYQLHRYAPQ QQQQHILLSS
301 GSSSSKHNSN NNSNTSAGAA SAAVPIATSV AAVPTTGGSL PDSPAHEHS HESNSATASA
361 PTTPSPAGSV TSAAPTATAT AAAAGSAAAT AAATGTPATS AVSDSNNNLN SSSSSNSNSN
421 AIMENQMALA PLGLSQSMDS VNTASNEEEV RTLKVSGLPM DAKPRELYLL FRAYEGYEGS
481 LLKVTSKNGK TASPVGFVTF HTRAGAEAAK QDLQGVRFDP DMPQTIRLEF AKSNTKVSKP
541 KPQPNTATTA SHPALMHPLT GHLGGPFFPG GPELWHHPLA YSAAAAAELP GAAALQHATL
601 VHPALHPQVP VRSYL

Figure 20. Expression of a human *cpo* homolog in mammalian (human) tissue

Quantitative analysis of RNA binding protein with multiple splicing (RBPM5) expression in human abdominal adipocyte cells during the differentiation from preadipocytes to mature adipocytes

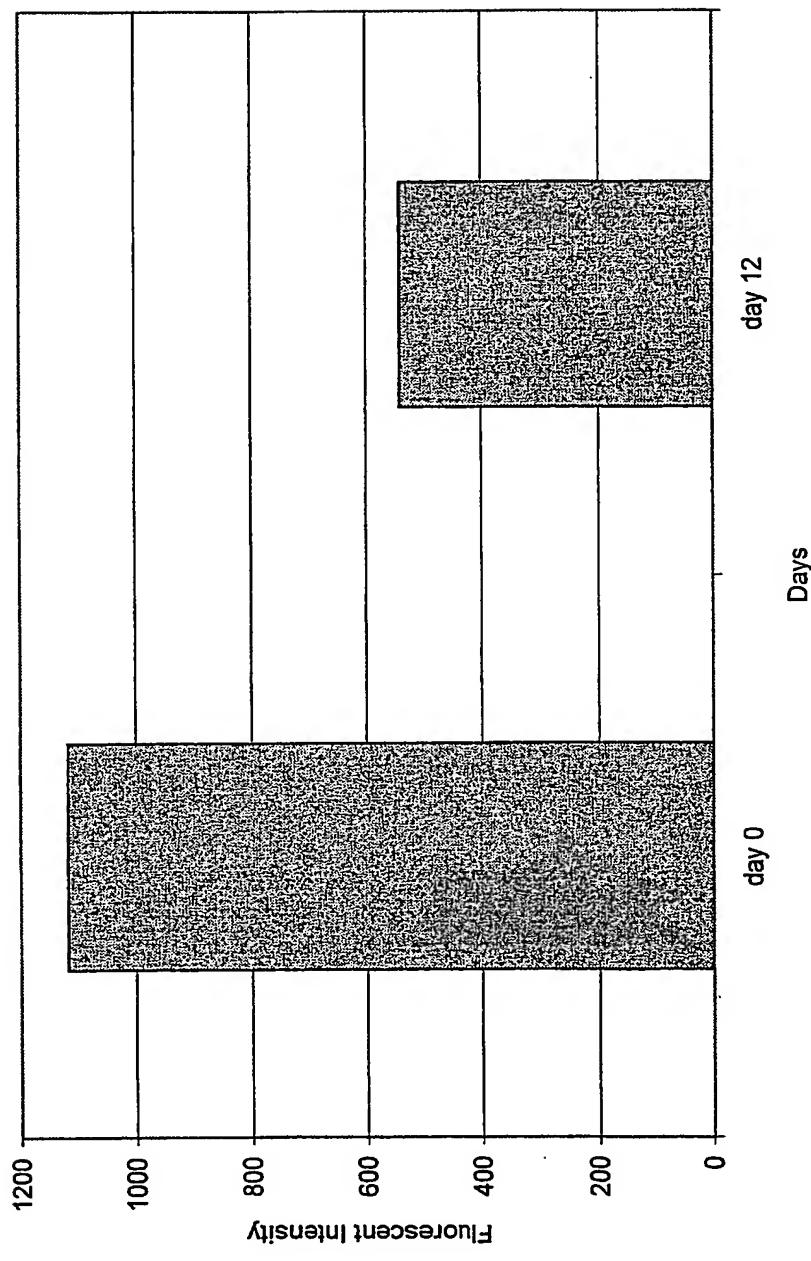


Figure 21. Triglyceride content of a *Drosophila Jafracl* (GadFly Accession Number CG1633) mutant

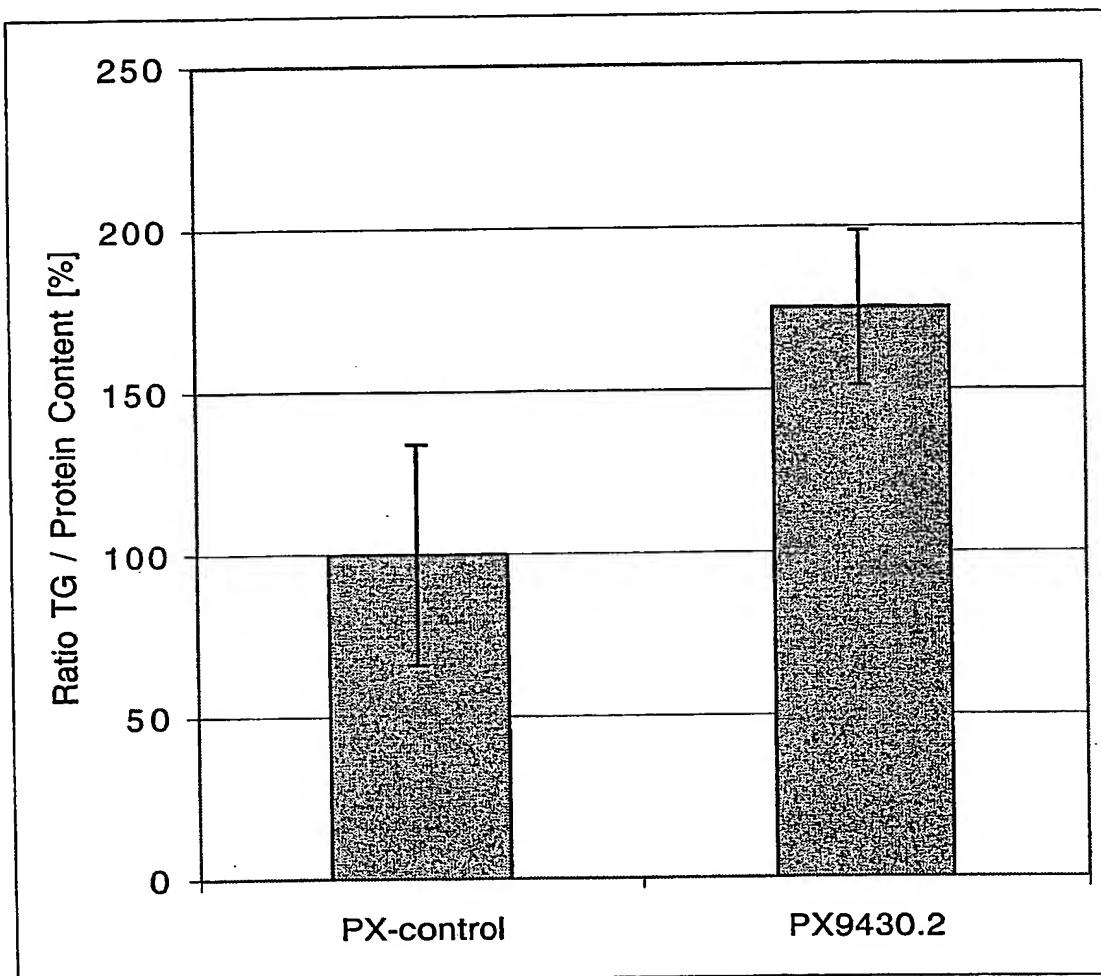


Figure 22. Molecular organisation of the *Jafracl* gene (GadFly Accession Number CG1633)

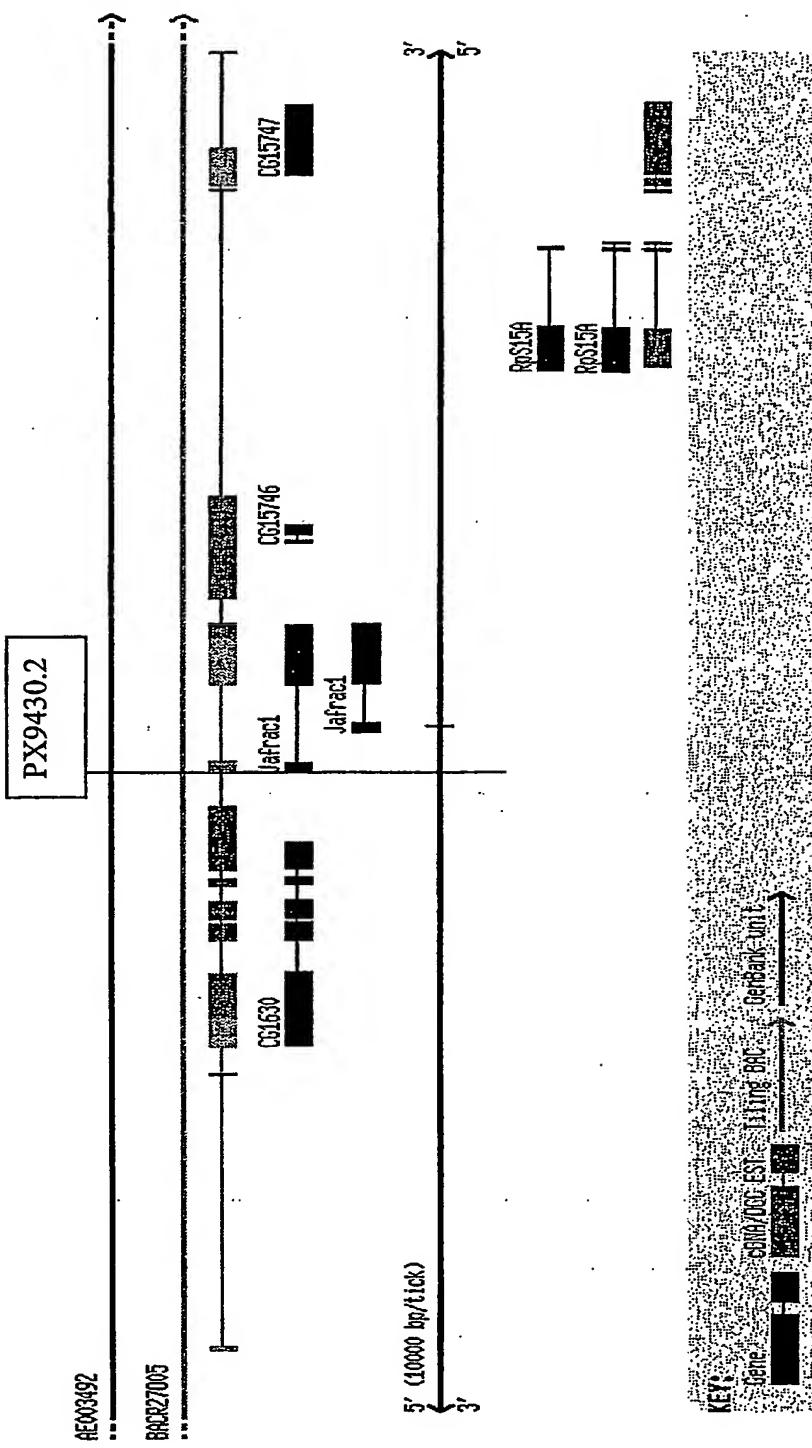


Figure 23. Homology of *Drosopila Jafrac1* (GadFly Accession Number CG1633) to human peroxiredoxin 1 and human peroxiredoxin 2 (similar to peroxiredoxin 1)

**Figure 23A. BLASTP results for *Jafrac1*
Homology to human protein XP_009063.2 (GenBank Accession Number)**

ref|XP_009063.2| (XM_009063) peroxiredoxin 2 [Homo sapiens]
Length = 198

Score = 283 bits (723), Expect = 9e-76

Identities = 134/188 (71%), Positives = 157/188 (83%)

```

Query: 3   QLQKPAPAFAGTAVVNGVFKDIKLSDYKGKYLVLFYPLDFTFVCPCTEIIIAFSSESAAEFR 62
          ++ KPAP F TAVV+G FK++KLSDYKGKY+VLFFYPLDFTFVCPCTEIIIAFS A +FR
Sbjct: 7   RIGKPAPPDFKATAVVVDGAFKEVKLSDYKGKYVVLFFYPLDFTFVCPCTEIIIAFSNRAEDFR 66

Query: 63  KINCEVIGCSTDQSQFTHLAWINTPRKQGGLGSMDIPLLADKSMKVARDYGVLDDEETGIPF 122
          K+ CEV+G S DSQFTHLAWINTPRK+GGLG ++IPLLAD + + + DYGV + GI +
Sbjct: 67  KLGCEVLGVSVDSSQFTHLAWINTPRKEGGGLGPLNIPLLADVTRRLSEDYGVLKTDDEGIAY 126

Query: 123 RGLFIIDDKQNLRQITVNDLPVGRSVEETLRLVQAFQYTDXKYGEVCPANWKPQKTMVAD 182
          RGLFIID K LRQITVNDLPVGRSV+E LRLVQAFQYTDXKYGEVCPA WKPG T+ +
Sbjct: 127 RGLFIIDGKGVLQRQITVNDLPVGRSVDEALRLVQAFQYTDEHGEVCPAGWKPQGSDTIKPN 186

Query: 183 PTKSKEYF 190
          SKEYF
Sbjct: 187 VDDSKEYF 194

```

Homology to human protein NP_002565.1 (GenBank Accession Number)

ref|NP_002565.1| (NM_002574) peroxiredoxin 1; Proliferation-associated gene A;
proliferation-associated gene A (natural killer-enhancing factor A) [Homo sapiens]
ref|XP_001393.2| (XM_001393) peroxiredoxin 1 [Homo sapiens]
Length = 199

Score = 281 bits (718), Expect = 3e-75

Identities = 135/185 (72%), Positives = 154/185 (82%), Gaps = 1/185 (0%)

```

Query: 7   PAPAFAGTAVV-NGVFKDIKLSDYKGKYLVLFYPLDFTFVCPCTEIIIAFSSESAAEFRKIN 65
          PAP F TAV+ +G FKDI LSDYKGKY+V FFYPLDFTFVCPCTEIIIAFS+ A EF+K+N
Sbjct: 11  PAPNFKATAVMPDGQFKDISLSDYKGKYVVFYPLDFTFVCPCTEIIIAFSDRAEFKKLN 70

Query: 66  CEVIGCSTDQSQFTHLAWINTPRKQGGLGSMDIPLLADKSMKVARDYGVLDDEETGIPFRGL 125
          C+VIG S DS F HLA+NT+KQGGLG M+IPL++D +A+DYGV + GI FRGL
Sbjct: 71  CQVIGASVDSHFCHLAWVNTPKKQGGLGPMNIPLVSDPKRTIAQDYGVLKADEGISFRGL 130

Query: 126 FIIDDKQNLRQITVNDLPVGRSVEETLRLVQAFQYTDXKYGEVCPANWKPQKTMVADPTK 185
          FIIDDK LRQITVNDLPVGRSV+ETLRLVQAFQ+TDK+GEVCPA WKPG T+ D K
Sbjct: 131 FIIDDKGILRQITVNDLPVGRSVDETLRLVQAFQFTDKHGEVCPAGWKPQGSDTIKPDVQK 190

Query: 186 SKEYF 190
          SKEYF
Sbjct: 191 SKEYF 195

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Figure 23B. Multiple Sequence Alignment (ClustalW 1.83)

Jafrac1 Dm MP----OLQKAPAPAFAGTAVV-NGVFKDIKLSDYKGKYLVLFYPLDFTVCPTTEIIIAFS
PRDX1 Hs MSSGNAKIGHPAPNFKATAVMPDGQFKDISLDYKGKYVVFFFYPLDFTVCPTTEIIIAFS
PRDX2 Hs MASGNARIGKPAPPDFKATAVV-DGAFKEVKLSDYKGKYVVLFFYPLDFTVCPTTEIIIAFS

Jafrac1 Dm ESAAEFRKINCEVIGCSTD SQFTHLAWINTPRKQGGGLGSMDIPLLADKSMKVARDYGVLD
PRDX1 Hs DRAEEFKKLNCQVIGASVDSHFCHLAWVNTPKKQGGLGPMNIPLVSDPKRTIAQDYGVLK
PRDX2 Hs NRAEDFRKLGCEVLGVSVDSQFTHLAWINTPRKEGGLGPLNIPLLADVTRRLSEDYGVLK

Jafrac1 Dm EETGIPFRGLFIIDDKQNL RQITVNDLPVGRSVEETLRLVQAFQYTDKYGEVCPANWPG
PRDX1 Hs ADEGISFRGLFIIDDKGILRQITVNDLPVGRSVDETLRLVQAFQFTDKHGEVCPAGWPG
PRDX2 Hs TDEGIAYRGLFIIDGKGVL RQITVNDLPVGRSVDEALRLVQAFQYTDEHGEVCPAGWPG

Jafrac1 Dm QKTMVADPTKSKEYFETTS
PRDX1 Hs SDTIKPDVQKSKEYFSKQK
PRDX2 Hs SDTIKPNVDDSKEYFSKHN

Figure 24. Expression of a human *Jafracl* / homolog in mammalian (human) tissue

Quantitative analysis of Peroxiredoxin 1 (PRDX1) expression in human abdominal adipocyte cells during the differentiation from preadipocytes to mature adipocytes

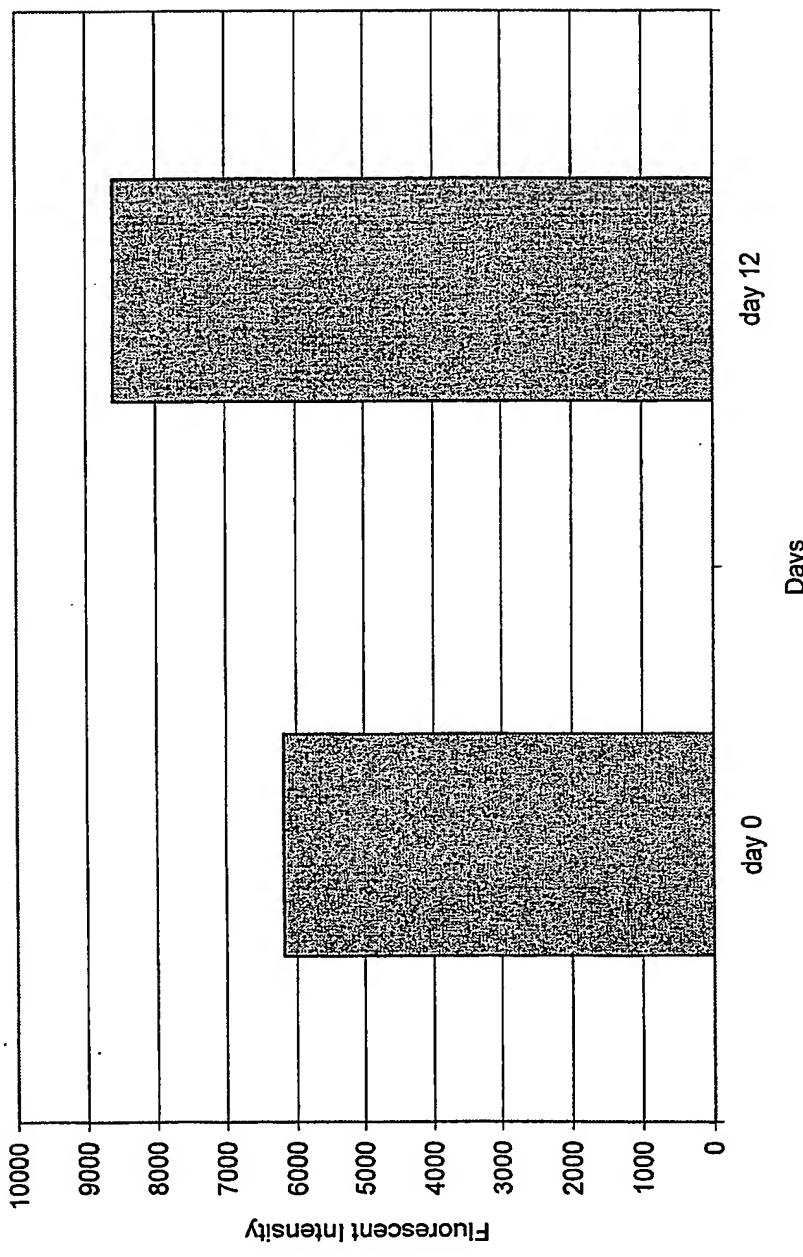


Figure 25. Triglyceride content of a Drosophila CG14440 (GadFly Accession Number) mutant

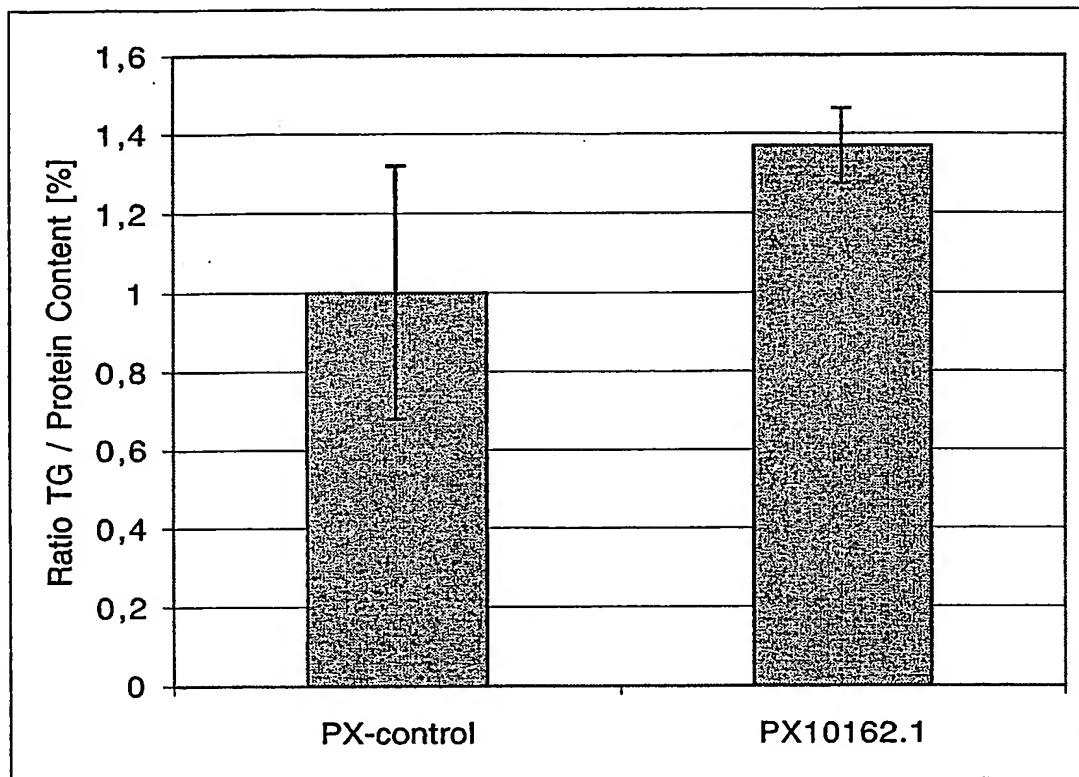
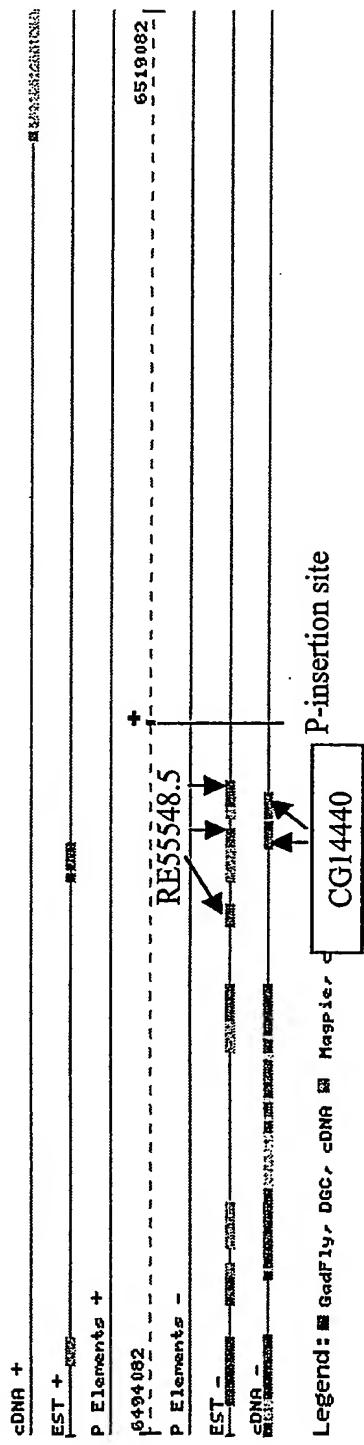


Figure 26. Molecular organization of the CG14440 gene (GadFly Accession Number)



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Figure 27. BLASTP results for CG14440 (GadFly Accession Number)

Homology to human protein NP_060000.1 (GenBank Accession Number)

ref|NP_060000.1| (NM_017530) hypothetical protein LOC55565 [Homo sapiens]
Length = 370

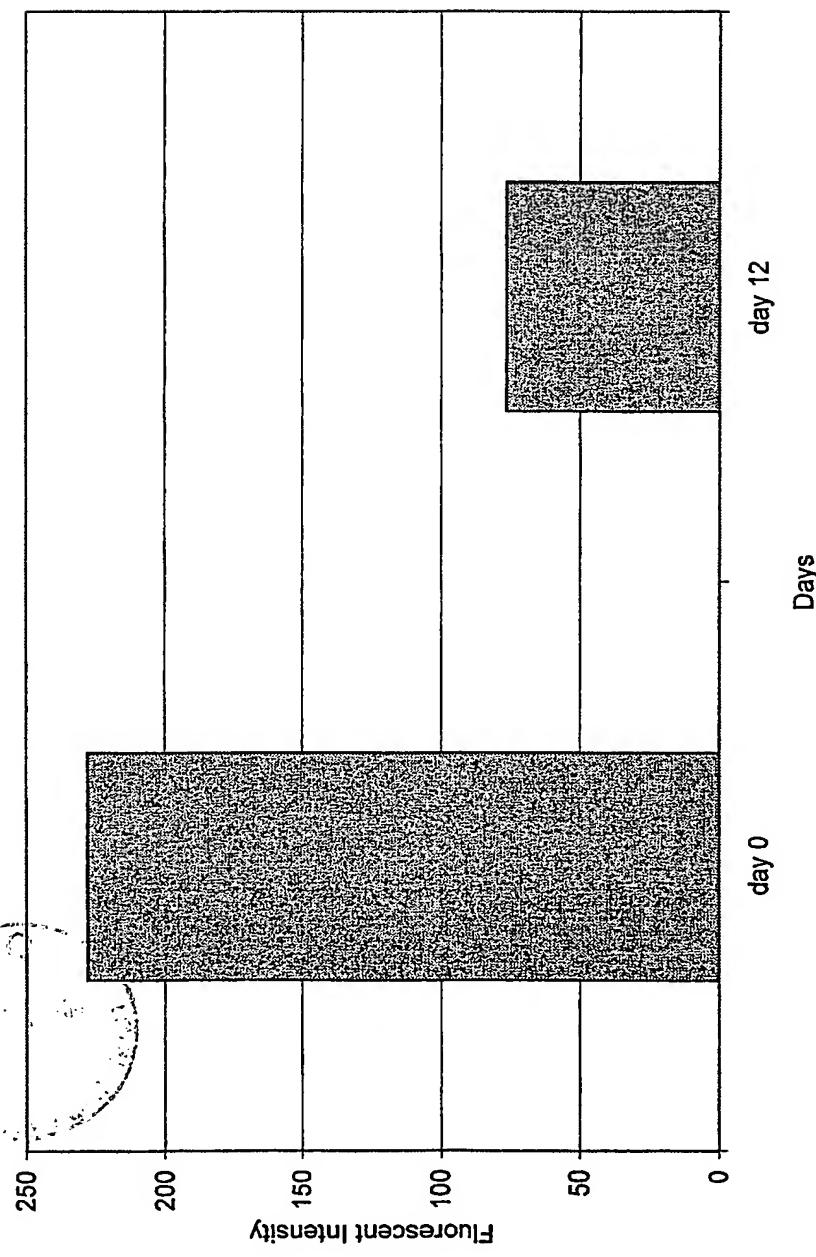
Score = 77.4 bits (189), Expect = 2e-13
Identities = 41/106 (38%), Positives = 62/106 (57%)

Query: 195 QQQSSRAQKAARRRSNESIEARERRLERNAARMRDKRAKESEAERYVRVLAKNAEANRVRR 254
+ Q+ +K A RR NE +E R +RLER + +R E+ E VR ++ EA R++R
Sbjct: 207 EAQTPSVRKWALRRQNEPLEVRLQLERERTAKKSRRDNETPEEREVRRMRDREAKRLQR 266

Query: 255 QNETEVQRTLRLMKNAARQLRRASETVEERKKRLAKAAERMRIAR 300
ET+ QR RL ++ RL+RA+ET E+R+ RL + E R+ R
Sbjct: 267 MQETDEQRARRLQRDREAMRLKTRANETPEKRQARLIREREAKRLKR 312

Figure 28. Expression of the human CG14440 homolog in mammalian (human) tissue

Quantitative analysis of human hypothetical protein LOC55565 expression in human abdominal adipocyte cells during the differentiation from preadipocytes to mature adipocytes



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